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FIGURE 75

CGGGTCTGATAGTCCCTACCTGTCAGGACTGGTGTAGGATGAGATAATGTTTGTGAAGTGTAAACATATATAA
 ACCTGTGCTACTGTGAGAACTGGACAAAGAAAGAGAGGGAGTGGAGAGAAATCAAGGGAGGGCTGGGGCTGGGAA
 AGAACGAAAAGGGAGTCCGCTATAGAGGAGAGGCGACAGTCCGAGCCACACTTTGCAATGAAACTCTTTAGAC
 TTTCTGCCGGGAGAGCGGGCCAGACGCGCCAGGTCTGTAGCAGGAGGCCGCGAGGGCGGGTCCCCAGAGCCCTA
 CAGGTGAGTATCGGTTCTCCCTTCCCGGCTTTCCGCTCCGAGGAGGCGGAGCAGCTTCCCTGTTCTGATCTCT
 ATCGCGGGCGGCGCAGGGCCGGCTTGGCTTCCCTGAGACGCGGGAGGGGGCGGGATGTGTACCCCAATACCA
 GTGGGGACGGTCCGTGGTGGAAACCGCCGGGCGAGTCCGGGTAGAGTATAAGAGCCGGAGGGAGCGGGCCGGGGCG
 CAGACGCTTCAGAGCCATCCCAAGACGCGGGAGCCCGAGCCCCGACGAGTCCCGCGGCTCATCGGCGGCGTCC
 GGTCCGCGCTTCTCCGCCCCACCATTGGCTCCGGGGCCCCGGCTTCCGCGCGCCACCGCTGCGGGCTGCCGCTCTG
 CTGCTGGTGTGGCGGCGGTGACCGGCGCACACGGCCGGCGCAGGACAACCTGCACGTGTCCACCAACAGATGAC
 CGTGTGCAGCCCGACGGCCCCCGGGCGGCGCTGCCAGTCCCGCGGCTGGGCTCGGGCATGGCGGTGACTGCT
 CCACGCTGAGCTCCAGCTGTCTGCTGCTCAAGGCGGGCATGAGCGCCCCCAAGAACCGCCGACGCTGGTGGCG
 CCGAGTGAGCAGCGCTCGTGGCAACGATGGCTCTACGACCCCCGACTGCGACCCCGAGGGCGGCTTCAAGGC
 GCGCCAGTGCAACCAAGAGCTCGGTGTGCTGGTGGTGAACCTCGGTGGGCGTGGCGCGCACGGAACAGGGCGAC
 TGAGGCTACGCTGCGATGAGCTGGTGGCGACCCACCAATCTCTATTGACCTGCGCCACCGCCCCACCGCCGGC
 GCGTTCAACCACTCAGACCTGGACGCGGAGCTGAGGCGGCTCTTCCGCGAGCGGTATCGGCTGCACCCCAAGTT
 CGTGGCGGCGGTGCACCTACGAGCAGCCCAACCATCCAGATCGAGCTGGGGCAGAACAGCTCTCAGAAAGCGCGG
 GTGAAGTGGATATCGGCGATGCGGCTACTACTTCGAGAGGGACATCAAGGGCGAGTCTCTATTCCAGGGCGCG
 GCGGCGCTGGACTTGGCGGTGCGCGGAGAACCCCTGAGGTGGAGCGCACGCTCATCTATTACCTGGACGAGAT
 TCCCCCGAAGTTCTCCATGAGCGGCTCACCGCGGCGCTCATCGCGCTCATCTGGTGGTGGTGGTGGGCGCTCG
 TCGCGGCGATGGCGCTCCTGGTGTACCAACCGGAGAAAGTCCGGGGAAGTACAGAAGGTTGAGATCAAGGAA
 CTGGGGGAGTTGAGAAAGGAACCGAGCTTGTAGGTACCGGCGGCGCAGGGGATGGGGTGGGGTACCGGATTTC
 GGTATCGTCCAGACCCAAGTGAAGTACGCTTCCCTGATCTCCGCGCAAGGAGAGCGTTTATCTTTCAAAAT
 CCTGCGTTCCCCCTCCCTTTTGGCAGACACACAGGTTTAAATAGATCTGCGCTCAGGGTCTCTCTTTCTCTCA
 CTTCTGTCTTGAGGGAAGCATTTCTAAAATGTATCCCTTTTCGGTCCACAAACAGGAAACCTGACTGGGGCAGT
 GAAGGAAGGCAATGGCAGCGTTATGTGTAAAAAACAGTATCTGTATGACAACCCGGGATCSTTTGCAAGTAA
 CTGAATCCATTTGGACATTGTGAAGGCTTAAATGAGTTTATGATGGGAAATAGCCTTGTATCGGCTGGGTTTA
 AATTATTTGATGAGTTCCACTTGTATCATGGGCTACCCGAGGAGAGAGAGGAGTTTGTAACTGGGCTATGTAG
 TAGCCTCAFTTACCATCGTTTGTATTACTGACCACATATGCTTGTCACTGGGAAAGAGCGCTTTTACGCTGCC
 TGAACGCAAGTTTGGATGTCTTTGAGGACAGACATTGCCCCGAAACTCAGTCTAFTTATTCTTCAGCTTGGCGTT
 ACTGCCACTGATATTGCTAATGTCTTTTGTGAAATGTTTGTACATATGTTGTCTTTGATATGTGTCTGTA
 ATTTTTTAAATAAAACACGANTTTAATAAATATGGGAAAGGCACAAACAGAGTCCGGCATTTGTGAAAAGT
 CCGTCCAGATTTCTATCACTTTGGTCTCTAAATTTCCCAAGACTTGTATTTTTTTTTTATTTCAAAATATAACAC
 TTTTTTTTCCCCAGAGTGGGTGTTTCTATGTGCTACTCTGGTGTGTCCCAAGATATCCTAACTGGCGAGTGT
 AAATGCTATTTCTTTCTAAATAAGATTATTTGGAAACCTTCTTCAAACTGCAGGAGGGGAGGCTCTGAGGGCAGG
 AGAAGCTAAAAGTACGTGCTTTTGTATGAAAAAGAGTCCAGTCTTTGGTCACTCTTAACAAAGGCTTATCACC
 ATGGAGACAGAAAAGTCTAGTTCAAGAGCTGTACCTCCTTGAATCCAGGCTTACTCGAAATAAGTGGTACTA
 TTTCCATTTAGCCTTTGAGCAAATCACTTAACTCAAAGCGCTTGTGGCTCTAAGATTAAAGGACTTT

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FIGURE 77

[illegible]

CCGCGCGGGCTCTCGCGCGGCGGGGACGCGCGGGGAGGATGCTGCTTGCGCGCGCCCGCGCTCCTCACCGTCTCT
CCGGGGCCCGCTGCTGGGGCTTTGTTGTGGCCCGGAAGCGCGCGGCGCCACCCCTGAAGTTCGGCTGGCCCGCGCG
CGCGCACCTAGCGGACGGCGGGCGGGCGCGCGCTGTGCCCGAGAGTTCGCGCGCTGTGCGCGGTGGTGGGTGCAG
GACTGGACCCACGGGCGCATTTGTGGGCCCCGCGCGCGGACGCCAGGACCAATGGGTGAACCCCGAGGAGGCTTT
GCTGGCCAAAGCGCGTGTGGATCACCAGAGAGGGCCAAACCATATCTTCATCTCTGACGGGAGGAGGCCACCGCG
GGATGAGAGGCGGGCGCGCGGCGGACTGGGGGGCTCTGGTGGGTACCOCTGATGTTGTGTTGGACTCCAGCGCC
CGGGTGCCTCCTTACCGAATCTTTTACCAGACTCCAGACTCCCTGGTCTACTGGACCATCGCCTGTGGTGGTTT
CAGGAAAGAAATCACTGAACACTGGCAATGGCTTSGACAAATCTCTTGACAGACTCTCCATCTTTGAAATG
AGAATGATATCACCACATTTGTGAGAGGAAAAATACAGGGCATCTTCGAGAAATACAACAAATCAATGATGTA
AAGGAAGATGATGACACGGGAGGTTTAAAGAAGGCCATTGTGAAATTTCATAGGCTGTTTGGGATGCCAGGGA
AGAGAAACTCGTCAACTATTACTCTTGCACTATTGGAGGGAGGTCCCCCTCAGGGTGGATGTACCTCA
GCATTAACCACTTTGCTTTATCTTTCTTATGGGAAGGGAAGCGAACTGTCATCCGGTGGGTAGACATC
ACTTAAGCTTGAGAGAAATGCCACCTGCTTCTGCTGATGTGATCAAAGTGAACACACGGTCCAGTGAGCATTT
CTTCTCTGATTTCTCAACATCAACGAGACCTTCAAGTTAATGGAGCAGCTTGCCAAACATAGCCATGAGGCAAC
CTTTAGACAAATGAGGGATTTGAACAAGATCGATCCCTGCCCAACTCAAAAGGAAATCTCCTAAAAAATGTCT
GCTCTAAAAACGTGATCTTGATGCCAGGGCAAGAGTGAAGATACCGTGCACTTTTCCGGCTGCCCAAGATGA
AAAAATAGATGGCCACACAGTGTCACTCTCTGGACTCCATTTAACAAATGCACATTTTGGGCGAGATGTTT
TGTCACAAATATACATCTGTTTACCAGCAAGGGAGGAACTTATGTACCTCATTATCCCCTCCGTGAGGTG
ACAAATGTGGAAAGGCAGACAGCTCCAGTGTGCTCCCCAGTCCCTTATCCATCAGCACCCGAAACAGGATGAC
CTTCTATTTGCCAACTTGAAGATAGAGACTTTCTAGTGCAGAGGATCTCAGATTTCTGCAACAGACTACTT
CCAAAATATATTTCTGACAAAGGATTTGCGAGGAAGTTACAACAGTTCCAGATGATGAGGTGACTCTCGACCCAGC
AGCTTCGTCTCTCTCAGGCCCGACAGAGAACGAGCTCTGATCTGATGGAGAGCGCCAGTTTAACTTAATGG
CAACGCGCTCCCCACAGCCACACAGACCTGATGACCATGTATCGCGGGCGGTCTCCCGAGGAGTTCAACCCGA
AATTGGCCAAAGAGTTTCTGAAAGAGCAAGCGTGGAAAGATTCACTTTGCTGAGTATGGCCAGGGATCTGCATG
TACCGCACAGAGAAACCGCGGGAGCTGCTGTTGAAGGGCATCCCGGAGAGCATGCGTGGGGAGCTCTGGCTGCT
GCTGTGAGTGGCATCAATGAGAGGGCCACACATCTCGGTACTATGAAGACTTGTGGAGAAATCCATGGGGA
AGTATATCTCGCCACGGAGGAGATTGAGAGGGATTTACACCGCTCCTTCCAGAAACACCCAGCTTTTCAGAA
GAAATGGCCATGCTGCACTAAGGAGACTCTAACAGCTTATGCTTTGAAATCCCAACATAGGGTATTTGCA
GGCCATGGAATATTGTCACTCTAGTCTGCTGCTTTATGCCAAAGAGGAGGAGACCTTTCTGGCTGCTTGGCGT
TGCTGTGAGCGCATGCTCCAGATTCTACAAACAGAGTTGTGGGTGCACTGGTGGACCAAGGTGTCTTTGAG
GAGCTAGCACGAGACTACGTCCACAGCTGTACGACTGCATGCAAGACCTGGGCGTGATTTCCACCATCTCCCT
GTCTTGGTTCTTCACACTATTTCTCAGTGTGATGCTTTTGAGAGTGCAGTTGTGGTTGTTGACTGTTCTCTCT
ATGAAGGAATTAAGTGATATTCAGTGGGCTAGCTGTGCTGGATGCCAATGTGGACAAACTGTTGAAGTGC
RAGGATGATGGGAGGGCCATGACCTTTTGGGAGGTATTTAGACAGTGTGACCAATGAAGACAGCACACTGCC
TCOCATCTCTCACTCCACTCCTTCTGCTCAGCGATGATGTGGAACCTTACCTGAGGTAGACATCTTTAGACTCA
TCAGAACTCTCCTACGAGAAATTCGGAACATCTCCGGGAGATTTGATTGAACAGATGAGATTCAACACAGAGACTG
AAAGTGATCCGACGCTGGAGGATACTACGAAACGCAACGTGGTACGAACTTGTGACAGAACTTCCTTTAC
CATTGATGAGCTGGAGAACTTTATGCTCTTTTCAAGGCAGAACATCTACCAAGCTCTACTGGGGCGGAGCA
GCAACGCGCTGGACCGGCATGACCCAGCTGCGCTTACCTGGAACAGTATCGCATGACTCTCGAGCACTTCAAG
GGAATGTTTSCITCTTTCTTTCTTGGCACTGTGGAATCTCTGACTCTGAGCTCTGAGCTCTGCTGCTGCTGCT
ATTAGATGAAATGGAGACTTTTGAATTAACTTCCGGAGATTGTCTCTGGCTGAGTGTGATGCCATGAGGAGT
ACCTCAGACGAGAGCTCAAACCTCTGTACAAATGCACCTCTTGGCTGAGCCATCTCTGATCAAGTGAACCA
GATTCTGCTTTTGAAGCAACTCAGTACTCTTTGAAGATATTACCCAGAAATGTACACATGTTGTTGATTGGA
TAGCAGAGGCAACAGGGTGCAGATGATGGCTTTGTACGGTGAGCCTAAAGGCAGACAAAGGGAGAGAGCAA
ATTCCCAAGAAATCGTAATATTTGAGACTGTGGACTCCAGAAATTAATCTAAGTCAAAGAAATCAAAGGAA
TTACCCRAATTAATCAGGGGCGAGTTCATGSACTGTSTAGACAAATGTATAACATGTTCAGGCAAGACCCAA
TGAGCAGGAGCTGTACCATGCCACGCGCAGCATGACCAAGCTCTGCTGGAGATTGGGAGTGGGAGTGGCAGTGGT
TCGTGGCCCGAGCTGCAAAAGGAGGGCGGGAGCGGAGGCGAGTGGGCGCTCTGCCACACAGGGCATCCAGGGCTG
CTCTTCCCCAAGAAAGGGCCAGGCGAGCTTACGTGCTGGAGTCTGTTGAGCCCTGCGCGCCAGCCTGGCCCC
CGACAGCGAGGAACACTCCTTGGAGGACAAATGGAGCACATCAAGCTGGAGGACTCTCGCCCCCGGACAAAG
GGGCTGCTCCTGCTGCTGATCTGACGCGACACCAAGGACGACAGCTCCATGCTCTCTCACTCGGCTGCTG
AGTGGCGGCTCCACAGAGGAGGACAAGCTGCACTGCGAGACATCGGAGAGGACGGTCTCTGCTGCGGAGCGG
CCAGGGCAGCGCGGCACTGCCCCGAGCACCAGCTGGAGCGGAGCTGGGCGCATCACTTTGAGCAGTTCCTGG
CCTGCTCTTAAGTGAAGCTGCGCTGCTCAAGTACTTTGACAGCCGCTGTGATGATGCCAGGATTAACAGT
GCAAAAAACATCCGGATGATGGGCAAGCCCTCACCTCGGCGAGTGAATGAAATCTCGGCCATGTCGGGCTG
ACACGGGGCGCTTCCCGGGGAGTGGGAGGAGAGGAGGGGAGGGATTTTTTATGTTCTCTCTGTTGAGTTTT
TTCTTTCTTTCTTTTAAATTAATATTTATTAGTACCTGGCTTGAAGCCTAGTGTTTTCATAATGTAAATCAAT
GAAACTGTTGGAGAAATATTTAAACACCTCAATGTAGCTATACACTCTTGTTCGGGAGGGGATTTAC
AGATACAGTGTATTTCTGAAATCTAAAAAACAAGAGATGAATCTGTGATGATGTGTGATATAACTT
ATTAATCTTGTCTGTGCTGTATACATGTTTAAAAATAAGTACTGTTTAATGCTAAGTAAGGCAGCACTCAT
TTCTGATTCAGGCTTTTAAATAAAATTAAGCTGTAAAGCAAAATGAAGGCCACAAATGCAAGACTGTTCTT

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FIGURE 78B

AAATGGBAGGCATAGTCAGCGAGGGTAAATCCTATACCACCTTTAGGAAGTATTAAAAATATTTTAAAGATTGGA
AATATATTTTCATAGAAGTCCTCTATTCAAAATCATATTTCCACAGATGTTCCOCCTTCAAAGGGAAAACATTTGGG
GTTCTAAACAGTTATGAAAGTAAGTCATTTTACATGATTCCAGAATAACACTTGTATTGACCAATTTAGACAG
ATACCAGACCANTTTTGCATTTAAGAAATTGTTCTGATTATTTACGTCAACTCATFAGAATTCAGTGAAAAGTA
ACAGTCTTTTGTACAGAGAAATCTGAAAGTAGCAGCAAGACAGAGGGCTCARGACAGGTTTTTGCTTTTGCTT
TGCTTTTGTTTTTGAAGAGTAAAGTACTGATGCTTCTGATACTGGATGTTTAGCTTCTTACTGCAAAAACAT
AAGTAAACAGTCAACTTTAOCATTTCCGTATTCTCCRTAGATTGAGAGAAATTTATACCACATATCCCATATGA
CCATCTTTCCATCAAAATCAATGTAGAGATAATGTAAACTGABAAAAAATCTGCAAGATATGTAACTGAATGTT
TAAAAACAGAACTTGTCACTTTATATAAAAGAATAGTATGCTCTATTTTCTGAATGGATGTGGAAATGAAAGC
TAGCGCACCTGCACCTTTGAATCTTGCTTCTTTTTTATTACTGTTATGATTTTGCTTTTACAGATGTTGGACG
ATTTTCTTCTGATTGTTGAATTCATANTCATGGTCTCATTTCCCTTGGCTTCTTTGGAATATTTCTTCAACA
CATTCCTTTATTTTATTATACATPGTGCTCCTTTTTTTAGCTATTGCTGCTGTTGTTTTTTATTCTATTTACAGG
ATGATTTTTAAACTGTCAAAATGAAGTAGTGTAAACCTCAAAATAGGCTAAATGTGACCAATAAAATACAGCAAA
TACTCAGATACAGCTTTTTATCTTTGTGCTTGAGTTCCCTGCCTAAGGAATAACATTTATTCTTTTGACAACTTTT
GCAGGGGAAATATATACAGGCAACCATTTTGATTAAAGTAAATAAATTTTATAGGCAACATATAGAGAGANNTA
CAATTTTGTATATCAATGACTATATTTAAAAATAAGGANTATAATTTGTTATCAGTTATCTAACTTAAATGCT
TATCCATAATGATCAGTGATATTACGCTTTTTTAAATATGCTTGTGG

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FIGURE 79

MRAAYLFILFLPAGLIAAGGQYDLDFLPFPDDEVQYTHYSDQIDNEFYDYDQEVTPRPSEHQFQFQSQQQVQQEV
IPAPTPEPGNAELEPTEPGPLDCREEQYFCTRLYSINRNPCKQCLNEVCFYSLRRVYVINKEICVKRTVCAHEELL
RADLCROKFSKCGVMASGLCQSVAAASCARSCGSC

Signal sequence.

amino acids 1-19

N-myristoylation sites.

amino acids 161-166, 167-172

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FIGURE 80

MAARFLPVSPARALLLALAGALLAPCEARGVSLWNEGRADEVVSASVRSGLWTFVKSFDSKNHPEVLNIRLQR
 ESKELIINLERNEGLIASSPTETHYLQDSTDVSLARNYTVILGHCYYHGHVVRGYSDSAVSLSTCSGLRGLIVFE
 NESYVLEPMKSATNRYKLFPAKKLSVRGSCGSHHNTFNLAARKNVFPPPSQTWARRHKRETILKATKYVELVIVA
 DNREFQRQCKDLEKVKQRLIETIANHVDFYRPLNIRIVLVGVEVWDMDKCSVSQDEFTSLHEFLEWRKMKLIF
 RKSHDNAQLVSGVYFQGTITIGMAPIMSMCTADQSGGIYMOHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQ
 MAVKGGCCTMNASTGYPPFMVFSSCSRKDLTSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEHCUCGEPE
 EGMNRCCNATPTCTLEKPDVAVCAHGLCCEDCQLKPACTACRDSNSCDLPEFCTGASPHCFANVYLHDGHSQCQDQD
 GYCNGICQTHEQQCVTLWGPAGKAPAGICFERVNSAGDEYGNCGKVSCKSSFAKCEMRDAKCGKIQCQGGASRP
 VIGTNAVSTETNIPLOQGGGRILCRGTHVYLGDDMPDPGLVLAGTKCADGKICLNRQCCQNISVFGVHECAMQCCHG
 RGVCNNRKNCHCEARWAPFFCDKFGFGSSTDGSPTRQADNQELTIGILVFTLCILAAAGFVVYLKRKTLIRLLFT
 NKKTILEKLRCVKRPSKPRGQPCQAHLGHLGKGLMKKFPDSYFPKDNPRRLQCCQNVDISRPLNGLNVPQFQS
 TQRVLPPLHRAFRAPSVPARPLPAKPALRQAQGTCKPFPFQKPLPADPLARTTLTHALARTFGQWETGLRLAP
 LRPAPQYPRQVPRSTHTAYIK

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 709-729

N-glycosylation sites.

amino acids 111-114, 149-152, 381-384, 452-455, 651-654

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 206-209, 730-733, 742-745

N-myristoylation sites.

amino acids 89-93, 103-108, 177-182, 180-185, 313-318, 343-348, 377-382,
 407-412, 423-428, 424-429, 524-529, 630-635, 635-640, 656-661, 668-673,
 694-699, 708-713, 712-717, 878-883

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 347-356

Disintegrins proteins.

amino acids 454-504, 410-460, 486-536

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FIGURE 81

MASRSMRLLLLLSCLAKTGVIGDILMRPSCAFGWFFYHKSNICYGYFRKLNRNWSDAEIECQSYGNGANLASILSLK
EASTIAEYISGYQRSQPIWIGLHDPQKROQWQWIDGAMYLYRSWSGKSMGGNKHCAETSSNNNFLTWSSNECNK
RQHFLCKYRP

Signal sequence.

amino acids 1-22

N-glycosylation site.

amino acids 50-53

N-myristoylation sites.

amino acids 64-69, 125-130

C-type lectin domain signature.

amino acids 129-154

Lectin C-type domain.

amino acids 47-156

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FIGURE 82

MATMENKVICALVLVSMLALSTLAEAQTETCTVAFRERQNCGFFGVTPSQCANKGCCFDDTVRGVPWCFYPNTI
DVFFERECEP

Signal sequence.

amino acids 1-24

N-myristoylation sites.

amino acids 45-50, 64-69

Trefoil (P-type) domain.

amino acids 30-71

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FIGURE 83

MLPQITPFLLLVSLNLVHGVFYARRYQTFTGIKGFLENTRKTQFFIPTYTIKSKGLAVRGEQSTPGFPAGPRGHP
 GPGSEFPCKPGYQSPGLQGEPEGLPGFPGPSAVGKPGVPGLPSEKPGERGPFYGFKGDVGPAGLPGRGPFPGFPPIPG
 PAGISVPCKPGQQGPTGAPGPRGTFSEKAGPGVPGMNGQNGEMGYGAPGRPGERGLPGFPQGPTGPSGFPVGVGR
 GENGVPQQPGIKDRGFFGEMGFPGFPQGPPGERGPEGTIGKPGAAGAPGQPGIIPGTNGLPGAPGTAGFPFGFP
 GFCKPGLPGLKGERGPAGLPGGPGANGEGQGPAGLPCKPGLTGFPGMMPQGPGKIPGSHGLPGPKGETGPAGPA
 GYPGAKGERGSPGSDGKPGYFGKPLDGPKNPGLPGPKGDPGVGGPGLPGFVGPAGAKGMPGHNGEAGPRGA
 PGTPGTRGPIGPPIEGFPGSGDPPGSPGPPGAGTATNGLNGPTGPPGFPGRGSPGSEFGLPGFPFGPPGQ
 AVMFEGPIKACQRPGLSGTPLVSAHQGVGTGMPVSAFTVILSKAYFAIGTPIPFKILYNRQQRHYDFRTGLFTCQ
 IPGIYYFSYHVVVKGTHVWVGLYKNGTFVMYTYDEYTKGYLDQASGSAIIDLTENDQVWLQLPNAESNGLYSSE
 YVHSSFSGFLVAPM

Signal sequence.

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 116-123

N-myristoylation sites.

amino acids 18-23, 276-281, 317-322, 350-355, 380-385, 415-420, 446-451,
 529-534, 548-553, 587-592, 613-618, 661-666

Amidation site.

amino acids 219-222

Clq domain signature.

amino acids 571-601

Clq domain.

amino acids 553-677

Collagen triple helix repeat (20 copies).

amino acids 92-150, 156-214, 223-281, 282-340, 344-403, 404-463, 464-522

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FIGURE 84

MEFLPPLLLLLLLAAPWGRAVPCVSGGLPKFANITFLSINMKNVLQWTPPEGLOGVKVITYTVQYFTYGGKKWLKNS
ECRNINRTYCDLSAETSDEYHQYYAKVKAINGTCKSKWAESGRFYPFLETQIGFPEVALTTDEKSISSVLTAFE
KWKRNFEULFVSMQQIYSNLKYNVSVLNTKSNRTWSQCCTNRTLVLTLWLEFNTLYCVHVESFVPGPPRRQAQSE
EQCARTLKQDSSEFKAKIIFWYVLPISITVFLFSVMGYSIYKYLHVQKEKHEANLILLYGNEFDKRFVPAEKI
VINFITLINISDDSKISHQDMSLLGKSSDVSSLNDPQPSGHLRFPQEEEEVENHLGYASHIMEIFCDSEHTEGTS
LTQQESLSKTIIPDKTVIEYEYDVRTDLCAGPEEQELSLQEEVSTQGTLLSQALAVLSPQTLQYSYTPQLQ
DLQPLAQEHTDSEEGPEEEPSTTLVDNDPQTGRLCIPSLSSFDQDSEGCCEPSEGDGLGEEGLLSRLYEAPAPDR
FPGENETYLQGFMEEWGLYVQMEN

Signal sequence.

amino acids 1-18

Transmembrane domain.

amino acids 239-259

N-glycosylation sites.

amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192, 304-307, 523-526

Tyrosine kinase phosphorylation sites.

amino acids 385-392, 518-525

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Phosphatidylinositol 3- and 4-kinases proteins.

amino acids 253-279

Tissue factor.

amino acids 1-278

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FIGURE 85

MFAPGRPALRFLPLPFLLLLLLLAAPWGRAVPCVSGGLPKFAMITFLSINMKNVLQWTFPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSQYEHQYYAKVSAIWGTKCSKWAESGRFYFFLETQIGFPEVALTTDE
KSISVVLTAPKWKRNPEELFVSMQQLYSNLKYNVSVLNTKSNRTWSQCVTNATLVLTWLEPNTLYCVHVESFV
FGPPBRAQPSKQCARTLKDQSSEFKAKILFWYVLPISITVFLFSVMGYSIYRYLHVKGKPKPAMLLIYGNF
DKRFFVPAEKIVINFITLNISSDQKISHQDMSLLGKSSDVSSSLNDFQPSGNLRPPQERREVKELGYASHLMEIF
CDSEENTECTSLTQOESLSRYIPDKTVLEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQAALAVLGFG
TLQYSYTPQLQULDFLAQEHDTSEEGFPEEPSTTLVDWDPQTGKLCIPSLSSFDQDSEGCEPSEGDLGEESLL
SRLYEEFAPDRPPGENETYLQFMEEWGLYVQMN

Signal sequence.

amino acids 1-29

Transmembrane domain.

amino acids 240-270

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FIGURE 86

MAAARLCISLLLLSTCVALLLQPLLGAQCAFLEFVYFGDNATPEQMAQYRADLRRIIMLTRPRYGRKKEDTL
AFSEWGSFHAAVPRELSFLDL

Signal sequence.

amino acids 1-29

N-myristoylation site.

amino acids 80-85

Amidation site.

amino acids 65-68

Pancreatic hormone family signature.

amino acids 49-65

Pancreatic hormone peptide.

amino acids 30-65

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FIGURE 87

MGPPSAPPFCRLHVPWKEVLLTASLLTFWNEPTTAKITIESTPFNVAEKGKVVLLLAHNLFPQMRIGYSWYKGERVD
GNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVITQNDTGFTTLOVIKSDLVNEEATGQFHVYPFLPKPS
ISSNNSNPVEDKDAVAFTCEPEVQNTTYLWVWNGQSLFVSPRIQLSNGNMTLTLLSVKRNDAGSYECETIQNPAS
ANRSDPVTNLNVLGPDGFTISPSKANYRPGENINLSCHAASNPPAQYSWFINGETFOQSTQELFIPNITVNNSGS
YMCQAENSATGLNRTVTMITVSGSAFVLCAVATVGTILEVLARVALI

Signal sequence.

amino acids 1-34

Transmembrane domain.

amino acids 322-342

N-glycosylation sites.

amino acids 104-107, 111-114, 115-119, 152-155, 173-176, 197-200, 224-227,
256-259, 274-277, 288-291, 292-295, 309-312

Tyrosine kinase phosphorylation site.

amino acids 206-213

N-myristoylation sites.

amino acids 85-90, 211-216, 295-300, 307-312, 332-337

Immunoglobulin domain.

amino acids 160-217, 252-301

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FIGURE 88

MELRVLLCWASLAAALEETLLNTKLETADLEKVVTFQVDGQWEELSGLDEEQHSVRYEVCDDVQRAFGQAHWLR
 TGWVPRRGAVHVVYATLRFTMLECLSLPRAGRSCKETTTFVYYESDAUTATALTFAWMENFYIKVDFTVAAEHLTR
 KRPGAEATGKVNVTLLKLGPLSKAGFYLAFCDDQACMALLSLHLFYKKCAQLTVNLTRFPETVPRELVVPVAGS
 CVVDVAVFAPGSPSPSLYCREDDQWAEQPVTCSCAPGFRAABGNTECRACAQQTFFKPLSGEGSCQPCFANSHSNT
 IGSAVCQCRCRVGYFRAPTDPRGAFCTTTPPSAPRSVVSRINGSSLELEWSAPLESSEGGREDITYALRCRECRPGGSC
 APCGGDLTFDPCPNLDVEPWVVVRGLRFDFTYTFEVTALNGVSSLATGFVFFEPVNVTTDREVFPAVSDIRVTR
 SSPSSLSLANAVPRAPSGAVLDYEVKYHEKGAEPSVVFLEKTSBNRAELRGLKRCASLYLVQVRARSEAGYGP
 GQEHHSQTOLDESEGWEQALIACTAVGVVVLVIVVAVLCLRKQSNGREAEYSKHKQYLLIGHTKVIYID
 PFTYEDPNEAVREFAKETDVSIVKLEEVIGAGEFGEVCRGRLKAPGKKESCVAKTLKGGYTERQKREFLSEAS
 IMCQFEHFNITRLEGVVTNSMFMILTEFMENGALDSFLRLNDGQFTVIQLVGMLRGIASCMRYLAEMSYVHRD
 LAARNILVNSNLVCKVSDPGLSRFLEENSSDFTYSSLGSKIPRWTAPEAIAFRKFTSASDANSYGIVMWEVM
 SFGERPYPWMSNODVINAIEQDYRLPPFPDCFTSLHQLMLDCWQKORNARFRFPQVVSALDKMIRNFASLKIVA
 RENGCASHPLLDQRQPHYSAFGSVGEWLRAIKMGRYEESFAAAGFGSFELVSQISAEOLLRIGVTLASHQKKIL
 ASVQBMKSQAKPGTGGTGGFAPQY

Signal sequence.

amino acids 1-15

Transmembrane domain.

amino acids 539-559

N-glycosylation sites.

amino acids 203-206, 335-338, 426-429, 768-771

Glycosaminoglycan attachment site.

amino acids 280-283

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 554-567, 639-642, 795-798

Tyrosine kinase phosphorylation sites.

amino acids 508-515, 588-596, 609-614, 729-736

N-myristoylation sites.amino acids 152-157, 182-187, 264-269, 298-303, 317-322, 374-379, 496-501,
681-686, 699-704, 719-724, 723-728, 951-956, 975-980**Amidation site.**

amino acids 637-640

Tyrosine protein kinases specific active-site signature.

amino acids 736-748

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FIGURE 89

MAQLFLPLLAALVLAQAPALADVLEGDSSSEDRAFRVPLAGDAPLQGVLCGALTFCHVHYLRPPPSRRRAVLGS
 PRVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTQVSLALSELRPNDUSGIYRCEVQHGIDSSD
 AVEVKVKGVVFLYREGSARYAFSFSGAQAEACARIGAHIAITPEQLYAAYLGGYEQCDAGWLSDDTVRYPIQTPRE
 ACYGDMDGFFGVNRYGVVDFDDLYDVICYAEDINGELFLGDFPEKLTLEEARAYQERGAELATTGQLYAANDG
 GLDHCSFPCWLADGSVRYPIVTPSQRCGGGLPGVKTFLFLEPNQTGFENKHSRFRNVYCFRDSAQPSAIPASNPAS
 NPASDGLAEIYTVTETLEELQLPQZATESESRGATYSTIFIMEDGGGGSSYPRDPAEAPRTILLEFETQSMVPTG
 FSEEEGKALENNEKYEDDEEEEEEEEEEEVEDEALWANFSELSSPGPEASLPTEPAAQEKSLSQAPARAVLQPG
 ASFLPDGSEASRPFRVGPPTETLPTFRERNLASPSSTLVEAREVGEATGGPELSCGVERGESEETGSSEGAP
 SLLPATRAPRGTRELEAPSEDNSGRTAPACTSVQAQFVLPTDSASRGGVAVVEASGDCVPSFCHNGGTCLEEEE
 GVRCLCLPGYGGDLCDVGLAFPCNPGWDAFQGAQYKHFSTRRSWEEAETQCRMVGAHLASISTPEEQDFINWRYR
 EYQWIGLNDRTIEGDFLWSDGVPLLYENWNFGQPDSTFLSGENCVMVMVWHDQSQWSDVPCNYHLSYTCRMGLVS
 CGEPPELFLAQVFGPRRLRYEVDTVIRYRCREGLAQRNLPLIRCQENGRWEAPQISCVPFRPARALHFEEDPEG
 RQGRLLGRWKALLTPSSSPMFGF

Signal peptide.

amino acids 1-15

N-glycosylation sites.

amino acids 130-133, 337-340

Tyrosine kinase phosphorylation sites.

amino acids 120-135, 451-459

N-myristoylation sites.

amino acids 47-52, 50-55, 133-138, 142-147, 174-179, 193-198, 281-286,
 298-293, 297-302, 324-329, 403-408, 414-419, 415-420, 576-581, 586-591,
 677-682, 684-689, 720-725, 772-777, 811-816

EGF-like domain cysteine pattern signature.

amino acids 670-682

C-type lectin domain signature.

amino acids 784-809

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 135-142

Link domain proteins.

amino acids 166-216, 264-314

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 655-676

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FIGURE 90

MAQLFLPLLAALVLAQAPAAALADVLEGGSSSEDAFRVRIAGDAPLQGVLGGAALTIFCHVHYLRPPFSRRRAVLGS
 PRVKWTFLSRGREAEVLVARGVVRVKVNEAYRFRVALPAYPASLTDVSLALSELRFNDSGIYRCEVQHGIDSSD
 AVEVKVKGVVFLYREGSARYAFSFSGAQAEACARIGAHIAITPEQLYAAYLGGYEQCDAGWLSQDTVRYPIQTRE
 ACYGDMDGFFGVNRNYGVVDPDDLYDVICYAEDLNGELFLGDPPEKLTLEEARAYCQERGAEIATTGQLYAANDG
 GLDHCSPGWLADGSVRYPTVTFSQRCCGGGLPGVKTLFLFENQTFGFFNKHSRFNVYCFRDSAQPSAIPASNEAS
 NPASDGLAIAIVTVTETLEELQLPQENTESERGAITYSIFIMEQGGGSSSTPEDPAEAFRTLLFETQGMVPTG
 FSHEEGKALEEEEEKYEDERKEEEEEEEEEVEDEALNWFSELSSPGPEASLPTEPAAQEESLSQAPARAVLQPG
 ASPLFDGESEASREPRVHGFFTTETLPTPREANLASPSSTLVEAREVGEATGGFELSGVPRGESEETGSSECAP
 SILPATPAPEGTRELEAPSEDNSGRTAPACTSVQAQPVLPYDSASRGGVAVVFPASGNSAQQGSTALSILILEFPL
 QLNV

Signal sequence.

amino acids 1-15

Transmembrane domain.

amino acids 652-670

N-glycosylation sites.

amino acids 130-133, 337-340

Tyrosine kinase phosphorylation sites.

amino acids 128-135, 451-459

N-myristoylation sites.

amino acids 47-52, 50-55, 133-138, 142-147, 174-179, 183-188, 281-286,
 288-293, 297-302, 324-329, 403-408, 414-419, 415-420, 576-581, 586-591

Immunoglobulins and major histocompatibility complex.

amino acids 135-141

Extracellular link domain.

amino acids 156-251, 257-353

Immunoglobulin domain.

amino acids 50-139

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FIGURE 91

MAVRQWVIALALALVVDREVFPVAAGKLEFGRMFICEHMMVESPTCSQMSNLVCGTDGLTYTNECQLCLARIKT
KQDIQIMKUGKC

Signal sequence.

amino acids 1-20

N-myristoylation site.

amino acids 50-63

Kasai-type serine protease inhibitor domain.

amino acids 37-86

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FIGURE 92

MAPLCPSFWLPLLIPAPAPGLTVQLLLSLLLLVPEVHFQRLPRMQEDSPLGGSSGEDDFLGEEDLPSEEDSFE
EDFPGEEDLPGEEDLPGEEDLPKPKSEEEGSLKLETLPTVEAPGDPQEFQNNASRDKEGDDQSHWRYGGDPP
WPRVSPACAGRFQSPVDIRPQLAAPCPALRPLELLGFLPFLPELRLNNHNSVQLTLPPGLEMALGPGREYRA
LQLHLHWGAAGRPGSEHTVEGHRFPAEIHVVHLSTAFARVDEALGRPGGLAVLAFLFEEGFEENSAYEQLLSRL
EEIAEEGSETQVPGLOISALLPSPDFSRYPFYEGLTTPFCAQGVITVFNQTVMLSAKQLHTLSDTLWGPQDSR
LQLNFRATQPIINRVIRASFPAGVDSSPRAAEPVQLNSCLAAGDILALVFGILLFAVTSVAFLVQMRBQHRGCK
GGVSYRFAEVAETGA

Signal sequence.

amino acids 1-37

Transmembrane domain.

amino acids 409-429

N-glycosylation site.

amino acids 346-349

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 440-443

N-myristoylation sites.

amino acids 50-55, 51-56, 209-214, 236-241, 310-315, 339-344, 421-426,
442-447

Eukaryotic-type carbonic anhydrases signature.

amino acids 237-253

Eukaryotic-type carbonic anhydrase.

amino acids 141-390

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FIGURE 93

MDALQLANSARAVDLFNQQLCEKEPLGNVLFSPICLSTSLSLAQVGAKGDTANEIGQVLHFNENVKDVFFGFQTVT
SDVNKLSSTFYSLKLIKRLYVOKSLNLSTFTSSTKRFPYAKELETVDKDKLEETKGGQINNSIKDUTDGHFENIL
ADNSVNDQTKILVVNAAYPVGNWKKKFSESETEKECPFRVNKTDTKPVQMRNMEATFCMGNIDSINCKTIELFFQ
NRHLSMFILLPKDVEDESTGLEKIEKOLNSESLSQWTNPSTMANAKVKLSLPKFKVEKMIIDPKACLENLGLKHI
FSEDTSDFSGMSETKGVALSIVLRKVCLEITEDGGDSIEVPGARILQHKUELNAOHPPFIYIIRHNETPNIEFFG
KFCSP

Signal sequence.

amino acids 1-42

N-glycosylation sites.

amino acids 99-102, 133-136, 188-191, 361-364

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 173-176

N-myristoylation sites.

amino acids 130-135, 207-212, 306-311, 312-317

Serpin (serine protease inhibitor).

amino acids 3-375

Fibrillarin proteins.

amino acids 150-169

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FIGURE 94

MDRHSSYIFIWQLQLCAMAVLLTRGETRCYCDAAHCVATGYMCKSELSACFSKILDPQNSNSPLTHGCLOSLA
STTDICQAKQARNHSGTTIPTLECCHEDMCNYRGLHDVLSPPRGEASGQGNRYQADGSRNLITKVQELTSSKEL
WFRAAVIAVPIAGGLILVLLIMLALRMLRSENKRLQDQRQOMLSRLHYSTFNGHHSKNGQVAKLDLECMVPVSGH
ENCCLTCDKMRQADLSNDKILSLVHWGMYSGEKLEFV

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 152-172

N-glycosylation site.

amino acids 87-90

Glycosaminoglycan attachment sites.

amino acids 121-124, 252-255

N-myristoylation sites.

amino acids 68-73, 249-254

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FIGURE 95

MNRRNDTLQSTRTRYSSASRSTDLSSSEDLVNFIOANFKKRECVFFTKDSKATENVCKCGYQSQHMEGTQI
 NQSEKWNYYKKHTKEFPTDAFGDIQFETLGKKKGHYIRLSCDTPARILYELLTQHWHLKTPMLVISVIGGAKNFAL
 KERMRKIFSRILIYIAQSKGAWILPGGTHYGLTKYLCEVVRDNTFISRSSEENIVAIGIRANGMVSNRDTLIRNCD
 ARGYFLAQYLMDDFTRDPLYILDNNETHLLLVONGCHGHFTVEAKLANQLEKHLISERTIQDSKYGGKIFIVCFA
 QGGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLVKFLPRTVSRLESEETESWIK
 WLKEITLCSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQDKDNWNGQLKLLLEWNQLDLANDEIFTNDRRW
 ESADLQEVMTALIKDRPKFVRLEFLNGNLNRKFLTHDVLTELEFSNHFTLVYRNLOIAKNSYNDALLTFVWKL
 VANFRGCFRKEDRNRDEMDIELHUVSPITRHFPLQALFIWAILQNKKELSKVIWEQTRGCTLAALGASKLLKTL
 AKVKNDINAAAGSEELANEYETRAVELFTECYSSDEDLAEQLLVYSCEANGGSCLELAVEATDQHFTAQPGVQ
 NFLSKQWYGEISRDTKNWKIILCLFIILPLVGC GFVSFRKKKPVDKRKKLLWYYVAFPTSFFVVFVSWNVVFXIABL
 LLFAYVLMDPFSVPHPPPELVLYSLVFVLEFCDEVRCQWYVNGVNYFTDLWNVMDTFLGLFYFIAGIVFRLSSNKS
 SLYSGRVIFCLDYLIIFTLELIHIFTVSRNLGPKIIMLQRLMIDVFFLEFLFAVWMVAFGVARQGLRQNEQRWR
 WIFRSVIYEFYLA MFGQVPSDVGTTDYDFAHCTFTGNESKPLCVELDENHLEPRFVENITIFLVCIYMLSTNILL
 VNLVAMEGYTVGVQENNDQVWKFGQRYFLVQEYCSRLNIPFPFVIFAYFYMVVKKCFECCCKERNMESSVCCF
 KNEDNETLAWEGVMKENYLVKINTKANDTSEEMRHRFPQLDTKINDLKGLLKEIANKIK

Transmembrane domains.

amino acids 691-701, 718-738, 734-754, 757-777, 784-804, 819-835, 853-873,
951-971, 995-1015

N-glycosylation sites.

amino acids 6-9, 75-78, 247-250, 308-311, 812-815, 925-928, 1041-1044,
1063-1066

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 83-86

Tyrosine kinase phosphorylation sites.

amino acids 21-27, 219-226, 279-286

N-myristoylation sites.

amino acids 71-76, 141-146, 174-179, 209-214, 299-304, 577-582, 643-646,
904-909

Amidation site.

amino acids 102-105

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FIGURE 96

MRNRKNDTLDSTRILYSSASRSTDLSESEDLVNFIQANFKKRECVEFTTKDSKATENVCKCSYAQSQHMEGTQI
 NQSEKWNYYKKHTKEFPTDAFGDIOFETLGKKKGKTYIRLSCDTDARILYELLTQHWHLKTENLVISVFGGARNFAL
 KPRMRKIFSRLLIYLAQSKGAWIITGGTHYGLMKYIGEVVRDNTISRSEENIVAIGIRAWGMVSNRDTLIRNCD
 AEGYFLAQYLMDDFTRDPLYILDNNETHLLLVDSNGCHGHPTVEAKLNQLEKYISERTIQDSNYGGKIPVCF
 QGGGKETLKAINITSIKNKIPCVVVEGSGQIADVIASLVEVEDALTSSAVKEKLVKFLPRTVSRLEETETESWIK
 WLKELLECSHLLTVIKMEEAGDEIVSNAISYALYKAPSTSEQDKDNWNGQLKLLLEWNQDLANDEIFTNDRW
 ESADLQEVMTALIKDRPKFVRLFLENGLNLPKFLTHDVLTELFSENHPSTLVYRNLIQAKNSYNDALLTFVWKL
 VANFRGGRKEDURNGRDEMDELHUVSPITRHPQLQALFIWAILQNKKELSKVIWEQTRGCTLAALGASKLLKTL
 AKVENDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLLVYSCEAWGGSNCLELAVEATDQHFLAQPGVQ
 NFLSKQWYGRISRDTKNWKIILCLFLIPLVGC GFVSFRKKFVDKHKLLWYVAFETSPFVVSWNVVFYIATL
 LLFAYVLMDPFSVPHPPPELVLYSLVFLFCDEVQWYVNGVNYFTDLWNVMDFLGLEFYTIAGIVERLESSNKS
 SLYSGRVIFCLDYIIFTLRLLHIFTVSRNLGPKIIMLQRMILIDVFFFLFLFAVWMVAFGVAPQGIILRQNEQRWR
 WIFRSVIYEPYLAMPQGVPSDVGDTTYDFACFTFYGMESKEFLCVELDERNLPRFPENITFLVCIYMLSTNILL
 VNLLVAMFGYTFVGTVOENNDQVWKEQRYFLVQEYCSRLNIPTFFIVFAYFYMVVKKCFKCCCKEKNMESSVCCF
 KNEDNETLAWEGVMKENYLVKINTKANDTSEEMRRRPRQLDTKLNDLKGILLKEIANKIK

Transmembrane domains.

amino acids 681-701, 718-738, 734-754, 757-777, 784-804, 819-839, 853-873,
 951-971, 995-1015

N-glycosylation sites.

amino acids 6-9, 75-78, 247-250, 308-311, 812-815, 925-928, 1041-1044,
 1053-1066

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 83-86

Tyrosine kinase phosphorylation sites.

amino acids 21-27, 219-226, 279-286

N-myristoylation sites.

amino acids 71-76, 141-146, 174-179, 209-214, 299-304, 577-582, 643-648,
 904-909

Amidation site.

amino acids 102-105

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FIGURE 97

RRGRGEVLAVERGSGSGGGGTRSGWFAAAGADKKPSRCGSGREGEGVSEGHKSMTELYELVWRVLAALLCLHR
TLTSWLRVRFPTWNNIWRCCRAASAAVLAPLGFTLRKPPAVGGRNRHHNHPGGSCLAAAHHRMRWRADGRSL
EKLFPVHMGVLITEVREQEPSFSUIASLVVWCMVGCISYISVYDHQGTFRNNSKLMDEILKQQQELLGLDCSKYS
PEFANSNDKDDQVLNCHLAVKVLSPEDGSKADIVRAAQDFCQLVAQKQRRTDLDVDTLASLLSSNGCPDPLVL
KFGPVDSTLGFPLPWIRLLEIVSLFSLNISTEDFFSALRQYAACEQRLGX

Transmembrane domain.

amino acids 166-186

N-glycosylation sites.

amino acids 198-201, 325-328

Glycosaminoglycan attachment sites.

amino acids 14-17, 16-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 34-37, 270-273

N-myristoylation sites.

amino acids 13-18, 15-20, 17-22, 19-24, 20-25, 47-52, 129-134, 156-161,
215-220

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FIGURE 98

MTGLYELVWRVLIHALLCLHRTLTSLRVRVFGTWNWINECCRAASA AVLAPLGFTLRKPPAVGNNRRHHRHPRG
GSCLA AAHHRMWRADGRSLEKLPVHMGLVITEVEQEFSFSDIASLVVWCMVGLSYLSVYDHQGIFFRMNSKL
MDEILKQQQELLGLDCSKYSPEFANGNKKDDQVLNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLD
VDTLASLLSSNGCEPDLVLKEGPFVSTIGFLPWHIRLTETIVSLPSHLNISYEDFFSALPQYAACEQRIGK

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 115-132

N-glycosylation sites.

amino acids 144-147, 271-274

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 216-219

N-myristoylation sites.

amino acids 75-80, 102-107, 161-166

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FIGURE 99

MVQRLWVSRLLRNRKAQLLELVNLTFTGLEVCLAAGITYVPFLLEVGVEEKFWMTMVLGIGFVLGLVCVFLQSA
SDHWGRGRYGRRRRFFIWALSLGILLSLFLIFRAGWLAGLICPDPRPLRLALLILGVGLLDFCGQVCFTPLEALLS
DLPRDPDHCRQAYSVYAFEMISLGGCLGYLLPAIDWETSALAPYLGTQEECLFGLLTILFLTCVAATLLVABEAA
LGPTEFAEGLSAPSLSPHCCPCRAKLAFRNLGALLPRLHQLCRMPRTLRLFLVAELCSWMAIMTFTLEYTDFV
GEGLYQGVPRAEPCTEARRHYDEGVRMGSLGLEFLQCAISLVFSLVMDRLVQRFCTRAVYLASVAAPFVAAGATC
LSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGGASSEDLSMTSFLPGPKPGAPFPNG
HVGAGGSGLLPPFPALCGASACVSVRVVVGEPTKRVVEGRGICLDLAILDSAFLLSQVAPSLFMGSIYQLSQ
SVTAYMVSNAAGLGLVAIYFATQVVFDKSLAKYSA

Signal sequence.

amino acids 1-35

Transmembrane domains.amino acids 15-35, 52-72, 87-107, 122-142, 160-180, 240-260, 277-297,
321-341, 486-506, 521-541**N-myristoylation sites.**amino acids 27-32, 95-100, 171-176, 299-304, 303-308, 320-325, 419-424,
447-452, 462-467**Amidation site.**

amino acids 82-85

Cell attachment sequence.

amino acids 415-417

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FIGURE 100

MALRRLLGAAILLLLPLLAAVEETIMDSITTATAELGWMVHFFSGWEEVSCYDENMNTIRTYQVCNVFESSQNNWLR
 TKFIRRRGAHRRIHVEMKFSVRDCSSIPSVPGSCKETFNLYYYEADFDSATKTFPNWMENFWVKVDTIAADESFS
 QVDLGGRVMKINTEVRSEGEVSRSGFYLAQDYGGCMBLIAVRVIFYRKCPRTTONGRAIFQETLSGAESTSLVAA
 RGSCLANAREVDVPIKLYCNGDGEWLVPICRCMCKAGFEAVENGTVCGCCPSGTFFKANQGDEACTHCPINSRTT
 SEGATNCVCRNGYYRADLDPLDMPCFTTIPSAFQAVISSVNETSLMLEWTPPRDSGGKEDLVYNTICKSCGSGRG
 ACTRCGDNVQYAPRQLGLTEPRIYISDLLAHTQYTFELQAVNGVTDQSPFSFQFASVNITTNQAAFSAVSIMHQ
 VSRIVDSITLSWSQPDQFNGVILDEYELQYYEKELSEYNATAIKSEPTNTVTVQGLKAGAIYVFQVRARTVAGYGR
 YSGKMYFQEMFEAEYQTSIQEKLPLTIIGSSAAGLVFLIAVVVIAIVCNRRRGFERADSEYTDKLOHYTSGHMTF
 GMKIYIDPFETYEDPNEAVREFAKEIDISCVRIEQVIGAGEFGEVCSGHLKLPKRETFVAIKTLKSGYTEKQRR
 DFLSEASINGQFDHFNVIHLEGVVTKSTPVMIIITRFMENGSLDSFLRQNDGQFTVIQLVGMLEGLAAGMKYLAD
 MNYVHRDLAARNILVNSNLVCKVSDUGLSRFELEDDTSDFTYTSALGGKIFIRKTAPEAIQYRKFTSASDVWSYG
 IVMWEVMSYGERFYWDMTNQDVINAEQDYRLPFPMDCPALHQLMLDCWQKDRNHRKPKFGQIVNTLDKMIKRN
 NSLKAMAPLSSGINLPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFQVVSQMMMEDILRVGLTLA
 GHQKKILNSIQVMRAQMNQIQSVEV

Signal sequence.

amino acids 1-18

Transmembrane domain.

amino acids 542-562

N-glycosylation sites.

amino acids 265-268, 336-339, 428-431, 482-485, 705-708

Glycosaminoglycan attachment site.

amino acids 367-370

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 802-805

Tyrosine kinase phosphorylation sites.

amino acids 374-381, 595-603, 736-743

N-myristoylation sites.

 amino acids 182-187, 213-218, 224-229, 271-276, 275-280, 299-304, 366-371,
 497-502, 546-551, 706-711, 726-731, 730-735, 875-880, 958-963

Amidation site - amino acids 644-647

Tyrosine protein kinases specific active-site signature - amino acids 743-755

Receptor tyrosine kinase class V signature 1 - amino acids 182-198

Receptor tyrosine kinase class V signature 2 - amino acids 241-261

Ephrin receptor ligand binding domain - amino acids 20-197

Protein kinase domain - amino acids 622-881

Fibronectin type III domain - amino acids 325-421, 436-520

SAM domain (Sterile alpha motif) - amino acids 912-976

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FIGURE 101

MALPRLGAALLLLPLLAVERETLMDSTTATAELGWMVHPPSCWEEVSGYDENMNTIRT YQVCHVFESSQNNWLR
 TKPIRRRGAAHRIHVEMKFSVRDCSSIPSVFGSCKETFNLYYYEADFDSATKTFPNMMENFWVKVDTIAADESFS
 QVDLGGVRVMKINTEVRSEFGFVSRSGFYLAQQDYGGCMSLIAVRVFPYRKCPRI IQNGAIFQETLSGAESTSLVAA
 RGGCIANAEEVDVPIKLYCNGDGEWLVPIGRMCCKAGFEAVENGTVCRGCPSGTFFKANQGDEACTHCPINSRTT
 SEGATNCVCRNGYYRADLDPLDMFCTTIPSAPQAVISSVNETSLMLEWTFPRDSGGREULVYNIICKSCSGRG
 ACTRCGDNVQYAPRQLGITEPRIYISDLLANTQYTFETQAVNGVTDQSPFSPQFASVNTITNQAPSAVSTIMEQ
 VSKTVDSITLSWSQPDQPNGVILSYELQYYEKELSEYNATAIKSPNTTFTVQGLKAGAIYVFQVRANTVAGYGR
 YSGKMYFQMTTEAENQTSIQEKLFLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTKLQHYTSCHMTFG
 MKYIYDPTTYEUPNEAVREFAKEIDISCVKIBQVIGAGEFGEVCSGNLKLPGKPELFAIKTLKSGYTEKQNRD
 FLSEASIMQQFDHPNVIHLEGVVTKSTPVMILITEFMENGSLDSFLRQNDGQFTVIQLVGMRLGIAAGMKYLADM
 NYVHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDDPTYSALGGKIPKWTAPRALIQYRKFTSASDVWSYGI
 VMWEVMSYGERPYPDWTNQDVINAIEQDYRLPPPMDCPFSAHQMLDCCWQKDRNRHPKFGQIVNTLDKMIKRNPN
 SLKAMAPLSSGGINLPLLDRTIFDYTSFNTVDWLEAIKMGQYKESFANAGTSTFVVVSQMMMEILRVGVTLAG
 HQKKIILNSIQVMRAQMNQIQSVEV

Signal sequence.

amino acids 1-18

Transmembrane domain.

amino acids 543-563

N-glycosylation sites.

amino acids 265-268, 336-339, 428-431, 482-485, 704-707

Glycosaminoglycan attachment site.

amino acids 367-370

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 801-804

Tyrosine kinase phosphorylation sites.

amino acids 374-381, 594-602, 735-742

N-myristoylation sites.amino acids 182-187, 213-218, 224-229, 271-276, 275-280, 299-304, 366-371,
497-502, 546-551, 705-710, 725-730, 729-734, 874-879, 957-962**Amidation site.**

amino acids 643-646

Tyrosine protein kinases specific active-site signature.

amino acids 742-754

Receptor tyrosine kinase class V signature 1.

amino acids 182-198

Receptor tyrosine kinase class V signature 2.

amino acids 241-264

Ephrin receptor ligand binding domain.

amino acids 20-197

Protein kinase domain.

amino acids 621-880

Fibronectin type III domains.

amino acids 325-421, 436-520

SAM domain (Sterile alpha motif).

amino acids 911-975

Src homology 2 (SH2) domains.

amino acids 733-769, 787-797, 806-819

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FIGURE 102

MNFSTSSSSSFAYDREFLRTLPGFLIVAEIVLGLLVSTLIAGTEYFRVFAFGWVMFVAVFYWVLTIVFFLIYYITM
TYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASSVSFERDSHNFNNSWAASSFFAFLVNICYAGNTYF6FIANK
SRTIQ

Signal sequence.

amino acids 1-41

Transmembrane domains.

amino acids 53-73, 86-106, 122-142

N-glycosylation sites.

amino acids 2-5, 92-95

N-myristoylation site.

amino acids 88-93

Leucine zipper pattern.

amino acids 17-38

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FIGURE 103

MNFSTSSSSFRYDREFLRLPGFLIVAEIVIGLLVWTLIAGTEYFRVPAPFGWVMFVAVFYWVLTVFELIITYTM
TYTRIPQVPWTFVGLCFNGSAFVLYLSAAVVDASSVSPERDSHNFNSWAASSFTAFLVFICYAGNTYFSFIAR
SRPIQ

Transmembrane domains.

amino acids 19-39, 53-73, 86-106, 122-142

N-glycosylation sites.

amino acids 2-5, 92-95

N-myristoylation site.

amino acids 88-93

Leucine zipper pattern.

amino acids 17-38

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FIGURE 104

MPTTVDDVLEHGGEFHFQKQMFELLALLSATFAPITYVGIVFLGFTPDHRCRSPGVAELSLRCGWSFAEELNYT
 VPGPGPAGEASPRQCRRYEVDWNNQSTFDCVDPLASLDTNRSRLPLGPCRDGWVYETPGSSIVTEFNLVCANSWM
 LDLFQSSVNVGFFIGSMSICYIADRFGRKLCCLTTVLINAAAGVLMALSPITYTWMLIFRLIQGLVSKAGWLIQY
 ILITEFVGRRYRRTVFGIFYQVAYTVGLLVLAGVAYALPHNRWLQFTVALPNFFFLYYNCIPESFRWLISQNK
 AEAMPITKNTAKKNGKSLPASLQRLRLREETGKKLNFSEFLDLVRLTPQIRKHTMILMYNWFSSVLYQGILIMMG
 LAGDNIYLDFFYSALVEFPAAFMILITIDRIGKRYTWAASNMVAGAACLASVPIPGDLQWLKILISCLGRMGIT
 MAYEIVCLVNARLYPTFIRNLGVEICSSMODIGGIIITPFLVYRLTNIWLELPLMVFGVLGLVAGGLVLLLPEPK
 GKALPETTEARENMQRPKKNKEKMIYLOVQKLDIPLN

Transmembrane domains.

amino acids 20-40, 174-194, 205-225, 238-258, 269-289, 361-371, 376-396,
412-432, 492-512

N-glycosylation sites.

amino acids 72-75, 97-100, 113-116

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 345-348

Tyrosine kinase phosphorylation site.

amino acids 536-553

N-myristoylation sites.

amino acids 191-196, 254-259, 442-447, 466-471, 504-509

Amidation site.

amino acids 174-177, 229-232, 327-330, 401-404

Sugar (and other) transporter.

amino acids 23-529

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FIGURE 105

MPTTVDDVLEHGGEFFHFQKQMFILALLSATEAFTYVGIVFLGFTPDHRCRSPGVAELELRCSWSPAEELNYT
 VFGPGPAGEASFRQCRRYEVDWNQSTFDCVDPLASLUTNRSRLPLGPCRDGWVYETPGSSIIVTEFNLVCANSWM
 LELFQSSVNVGFFPGSM3IGYIADRFGKRLCLLTTLVLAAGVLMASPTTYTWMLIFRLTQGLVSKAGWLG
 ILLETFVGRKRYKRTVGIIFYQVAYTVGLLVLAGVAYALPHWRWLQFTVSLPNFFFLLYWCIPESFRLISQKN
 AEAMRIKHIAKKNGKSLPASLQRLRLBEETGKKLNPSFLDLVETPQIRKNTMILMYNWETSSVLYQGLINEM
 LAGDNIYLDFFYSALVEFFRAFMIIITIDRIGRRYPWAASNWVAGAACLASVFIPGDLQWLKIIISCLGRMGIT
 MAYEIVCLVNAELYPTFIRNLGVRICSSMCDIGGLITPFLVYRLTNWLELPLMVEGVGLVAGGLVLLLPETK
 GKALPETIRAEENMQPPKKEKMTYLVQVQKLDIPIN

Transmembrane domains.

amino acids 20-40, 174-194, 205-225, 238-258, 269-289, 351-371, 376-396,
 412-432, 492-512

N-glycosylation sites.

amino acids 72-75, 97-100, 113-116

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 345-348

Tyrosine kinase phosphorylation site.

amino acids 536-544

N-myristoylation sites.

amino acids 191-196, 254-259, 442-447, 466-471, 504-509

Amidation sites.

amino acids 174-177, 223-232, 327-330, 401-404

Sugar (and other) transporter.

amino acids 23-529

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FIGURE 106

MAPWPELGDAQPNFDKYLEGAAGQQFTAPDKSKETNKTENTEPVTKIELLPSYSTATLIDEPTTEVDDPWNLP
 LQDSGIKWSERDTHGKILCFPGGIGRLILLGLYFFVCSLDILSSAFQLVGGKMGAGQFTSNSSIMSNELLGLV
 IGVLVFVLVQSSSTSTSIIVVSMVSSSLTVKAAIFIIMGANIGTSITNTIVALMQVGDSEFRRAFAGATVHDF
 FNWLSVLVLLPVEVATHYLEIITQLLIVESFHFKNGEDAPDLLKVITTKFFTKLIVQLDKKVISQIAMNDEKAKNK
 SLVKINCKTFTNKTQINVTVPSTANCTSPSLCWTDSGIQNWTKMKNVTYKENTANCQHIFVNPFLFELAVGTILLI
 LSLVLVCGCLIMIVKILGSSVLGGQVATVIKKTINTDPPFFPAWLTGYLAAILVGAGMTFFIVQSSSVFETSALTPLI
 GIGVITIERAYPLTLGSGNIGTTTTAILAALASPGNALRSSQLALCHFFFNISGILLWYPIPFTRLPIRMAGKL
 GNISAKYRWFAVFYLIIPFFLLPLTVFGLSLAGWRVLVGVGVVVFITILVLCRLQLQSRCPVLPKCLQNNWF
 LPLWMSRLKFWDAVVSKEFTGCGFQMPCCYCCVCCCRACCLCGCPKCCRCCKCEDLEEAQEGQDVFPVKAPETFD
 NITISREAGCEVPASDSKTECTAL

Transmembrane domains.

amino acids 96-116, 136-156, 178-198, 219-239, 356-376, 372-392, 406-426,
 445-465, 488-508, 523-543, 549-569, 565-585, 592-612

N-glycosylation sites.

amino acids 36-39, 136-139, 298-298, 308-311, 313-316, 321-324, 335-338,
 340-343, 495-498, 520-532, 667-670

N-myristoylation sites.

amino acids 23-28, 79-84, 126-131, 131-136, 146-151, 150-155, 187-192,
 191-196, 393-398, 423-428, 460-465, 464-469, 519-524, 546-551, 634-639

4Fe-4S ferredoxins, iron-sulfur binding region signature.

amino acids 635-646

Insulin family signature.

amino acids 621-635

Heat-stable enterotoxins.

amino acids 617-633, 625-641, 613-629

Na⁺/Pi-cotransporter.

amino acids 118-549

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FIGURE 107

MAPWPELGDAQPNPDKYLEGAAGQQPTAPDKSKETNKTDNTEAFVTKIELLESYSTATLIDEPTENVDDPWNLP
 LQDSGTHWSEKDTKGKLLCFQIGIGRLILLGLFLYFFVCSLDILSSAFQLVGGKMGAGQFFSNSSIMSNPLGLV
 IGVLVTVLVQSSSTSTSIIVSMVSSSLTVRAAIFIINGANIGTSITNTIIVALMQVGRSEFRRAFAGATVHDF
 FNWLSVLVLLPVEVATHYLEIITQLIVESFHFNGEDAFDLLRVITKPFKLIIVQLDKKVISQIAMNDEKAKNK
 SLVKIWKCTFTNKTQINVTVFSTANCTSPSLCWTDCIQNWTMKNVTYKENIAKQHIQVNEHLPLDLAGVTILLI
 LSLVLVCGCLIMIVKILGSSVLKGVATVVKKTFINTDFFPPFAWLTGYLATLVGAGMTFIVQSSSVFTSALTPLI
 GIGVITIEKAYPLTLGSSNIGTTTTAILAALASPGNALKSSSLQIALCHFFFNISGILLWYFIPFTRLFIRMAKGL
 GNISAKYRWFVAVFYLIITFFFLIPLTVFGLSLAGWBVLVGVGVFVVFILILVLCRLQLQSRCPVLFKKLQNWNF
 LPLMRSLSKPWDVAVSKFTGCFQMRCCCCCKVCCCRACCLCGCPKCCRCCKCEDLEBAQEGQDVFPKAPETFD
 NITISREAQGEVPASDSKTECTAL

Transmembrane domains.

amino acids 96-116, 136-156, 178-198, 219-239, 356-376, 372-392, 406-426,
 445-465, 488-508, 523-543, 547-567, 563-583, 592-612

N-glycosylation sites.

amino acids 36-39, 136-139, 295-298, 308-311, 313-316, 321-324, 335-338,
 340-343, 495-498, 526-523, 667-670

N-myristoylation sites.

amino acids 23-28, 79-84, 126-131, 131-136, 146-151, 150-155, 187-192,
 191-196, 393-398, 423-428, 460-465, 464-469, 519-524, 546-551, 634-639

4Fe-4S ferredoxins, iron-sulfur binding region signature.

amino acids 635-645

Insulin family signature.

amino acids 621-635

Na⁺/Pi-cotransporter.

amino acids 118-549

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FIGURE 108

MWSGWNLWPLVAVCTADFFRDEAEKIMRDSFVIDGHNDLFWQLLDMFNNRLQDERANLTTLAGTHTWIPKLRAG
FVGGQFWVSVYTPCDTQNKDAVVRTLEQMDVVHRMCRMYPETFLYVTFSSAGIRQAFREGKVASLIGVEGGHSIDG
SLGVLRALYQLGMRYLTLTHTSCNTFWADNWLVDTGDSHFQSQGLSPFGQRVVKEINRLGVLIIDLAHVSVATMKA
TLQLSRAFVLFSSHSAYSVCASRRNVFDDVLRVLVKQTDLSLVMVNFYNNYISCTNKANLSQVADHLDRIKEVAGA
RAVGFGGDFDGVPRVPEGLEDVSKYFDLIAELLRRNWTEAEVKGALADNLLRVFQAVEQASNLTQAPEEEFIP
DQLGGSCRTHYGYSSCASSLRHHWGLLLASLAPLVLCISLL

Signal sequence.

amino acids 1-16

Transmembrane domain.

amino acids 392-410

N-glycosylation sites.

amino acids 57-60, 279-282, 332-335, 358-361

Tyrosine kinase phosphorylation site.

amino acids 110-118

N-myristoylation sites.

amino acids 63-68, 78-83, 124-129, 139-144, 151-156, 375-380, 395-400

Leucine zipper pattern.

amino acids 390-411

Renal dipeptidase active site.

amino acids 140-162

Renal dipeptidase.

amino acids 1-411

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FIGURE 109

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERS.LHAFMYLFLCMLAATDLALST
STMPKILALFWFDSREISFEACLTQMFFIHLSAIESTILLAMAFDRYVAICHFLRHAAVLNNTVTAQIGIVAV
VKGSLFFFPLELLIKRLAPCHSNVLSHSYCVHQDVMKLAYADTLPNVVYGLTALLVMGVDVMFISLSYFLIIR
TVLQLPSKSERAKAFGTCVSHIGVVLAIFYVPLIGLEVHREFGNSLHPFIVRVVMGDIYLLLPVIVNPIIYGAKTE
QIRTRVLAMFKISCDKDLQAVGSK

Transmembrane domains.

amino acids 26-46, 57-77, 96-116, 144-164, 197-217, 238-258, 272-292

N-glycosylation sites.

amino acids 5-8, 136-139

N-myristoylation site.

amino acids 18-23, 238-243, 245-250

7 transmembrane receptor (rhodopsin family).

amino acids 40-131, 212-291

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FIGURE 110A

MRILKRFLACIQLLQVCRILDWANGYYRQQRKLVEEIGNSYTGALNQKKNWGGKYPFCNSPKQSPINIDEDLEQVN
 VNLKKLKFGQWDKTSLENTPIHNTGKTVEINLTNDYRVSQGVSEMYFKASKITPHWGKCNMSSDGSSEHSLEGQK
 FPLEMQIYCFDADRFSFEEAVKGGKGLRALSTLFEVGTENLOPKALIDGVEVSRRFGKQAALDPFILLNLLP
 NSTDKYYTYNGSLTSPCTDTVDWIVFKDTVSISESQLAVFCEVLTMQSSGYVLMMDYLQNNFREQQYKFSRQV
 FSSYTGKEEIHAEVCSSEPEENVQADPENYTSLLVTWERPRVVDYDMTEKFAVLYQQLDGEDQTKHEFLTDGYQD
 LGAILNLLPNMSYVLIQIVAICTNGLYKYSQQLIVDMPTDNPELDLFPFELIGTEETIKKEEKGKUIEEGAIVN
 PGRDSATNQIRKKEPQISTTTHYNRIGTKYNEAKTNRSPTKGSFSGKGDVNTSLNSTSQPVTKLATEKUTSL
 TSQVTVELPPHTVEGTSASLNDGSKTVLRSPHMNLSGTAEASLNTVSIYEESLSTSPKLDTGARDSSGSSPA
 TSAIPIFISENISQGYIFSSENPETITYDVLIPESARNASEDSTSSGSEESLKDPSEMGVWFFSSTDTAQPDPV
 GSGRESFLQNTYETIRVDESEKTTKSFSAGPVMSCGFSVTDLEMPHYSTFAYFTEVTPHAFTPSSRQODLVST
 VNVVYSQTTQPVYNGETPLQPSYSSEVFELVTFILLDNQILNTTFAASSSDSALEATPVFPVSVVSFESILSSY
 DGAFLLPSSASFSSELEFRHLHTVSQLLPQVTSATESDKVPLHASLPVAGGDLLEPFLAQYSDVLSTTHAASE
 TSGPSESGVLYKTLMTFSQVEFPSSDAMHARSSGPEPSYALSDMEGSGHITFVSYSALPVDHDSVGVTYQGS
 FSGPSEHIPKSSSLITPTASILLQPTAALSGDGEWSSGASSDSEFLPDTGLTALNTSSPVSAEFTYTTTSVFGD
 DNKALSKSEIIYGNETELQIPSFNEMVYPSESTVMPNMYDNVKNLASLQETSVSISSTEGMFFGSLAHTTKV
 FDHEISQVFENNFSVQPTHTVSCASGDTSLKPVLSANSEPASSDPASSEMSPSTQLLFYETSASFSTEVLLOP
 SFQASDQVDTLLKTVLFAVPSPDFILVETPKVDKISSTMLHLIVNSASSENMLHSTSVPVFDVSPTHMHSASLQ
 GHTISYASEKEYEPVLLKSESHQVVPSELYSNDLEFQTANLEINCAHPEKGRHVEATFVLSIDEPIINTLINKLIH
 SDEILSTKSSSVTGKVEAGIFTVASDTFVSTCHSVPIGNHVAITAVSPHRDGSVTSTKLLFPSKATSELSHSA
 KSDASLGVGGEDGDDTDDGDDDDDDSDGLSIRKCMSCSSYRESQEKVMNDSOTHENSLMDQNNPISYSLSENS
 EEDNRVTSVSSDSQTMDRSPGKSPSANGLSQKHNDGKEENDTQTGSALLEPLSPESKANAVLTSDEESGSGQGT
 SDSLNEENETSTDFSADTNEKDADGILAAGDSEITPGFPQSPSTSSVTSSENSEVPHVSEAEASNSHESRIGLAE
 GLESEKKAVIPLVIVSALTFFICIVVLVGLIYWRKCFQTAHFYLEDSTSPRVLSTPPTFTFTSDDVGAIPIKH
 FPKHVADLHASSGFTEEFETLKEFTYQEVQSCVTVDLGITADSSNHFPDNKHKNRYINIVAYDHSRVKLAQLAEKDG
 KLPDYINANYVDGYNRFPKAYIAQGGPLKSTAEDFWRMIEWENVEVIVMITNLVEKGRKCDQYWPADGSEYGN
 VGPVVVHCSAGVGRGTGYTYIVLDSMLQQIQHEGTVNIIFGLKHIRSQNNYLQVTEEQYVFIHDTLVEALLSKETE
 VLDSEIHAYVNAIIPGPAGKTKLEKQFQLLSQSNIQSSDYSAALKQCNKERNRTSSIIFVERS RVGISSLSGE
 GTDYINASYIMGYQSNEFIITQHPILLATIKDFWRMIWDHNAQLVMIIPDQGNMAEDFVYWPKNKDEPINCESF
 KVTIMARENKCLSNZEKLLIQDFILEATQDDYVLEVRHFQCPKWPNDSPISKTFELISVIRKEEAAANDGCPMTV
 HDEHGGVTACTTCALTTLMHQLEKENSVDVYQVAKMINILMRPGVFADIEQYQFLYKVLISLVSTRQENPSTSL
 DSNCAALPDGNIARSLSLV

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 1638-1658

N-glycosylation sites.

amino acids 105-108, 134-137, 223-226, 232-235, 324-327, 381-384, 497-500,
 501-504, 582-555, 602-605, 629-632, 677-680, 1017-1020, 1050-1053, 1082-1085,
 1122-1125, 1456-1459, 1561-1564, 1617-1620, 1868-1871, 2051-2054, 2076-2081

Glycosaminoglycan attachment sites.

amino acids 490-493, 991-994, 1548-1551, 1550-1553, 2070-2073

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 1877-1890

Tyrosine kinase phosphorylation site.

amino acids 148-156

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FIGURE 110B**N-myristoylation sites.**

amino acids 139-144, 186-191, 372-377, 471-476, 486-491, 533-538, 555-560, 582-587, 588-593, 638-643, 893-898, 960-965, 1097-1102, 1259-1264, 1385-1390, 1411-1416, 1415-1420, 1549-1554, 1551-1556, 1553-1558, 1579-1584, 1625-1630, 1879-1884, 1935-1940, 2123-2128, 2225-2230, 2226-2231, 2230-2235

Amidation sites.

amino acids 49-52, 1831-1834

Tyrosine specific protein phosphatases active site.

amino acids 1930-1942

Protein-tyrosine phosphatase.

amino acids 1749-1990, 2047-2280

Eukaryotic-type carbonic anhydrase.

amino acids 30-300

Fibronectin type III domain.

amino acids 312-401

MAM domain proteins.

amino acids 1757-1785, 1060-1088, 1813-1853, 2047-2079

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FIGURE 111

MCARMAGRTTRAAPPGPYGFWLCLLVALALDVRVDCGQAPLDFVYLHVTAARPAQPTLWTAKLDRFKGSRHHTT
 LITCHRAGLTEPDSSSPLELSEFLWVDFVVENSTGGGVAVTRFVTWQLEYFGQAPEAEKDKMVNEILVSEDR
 ALIFLAKAEELVNTAFLTGVPQHVPVRLVTVDGGGALVEVTEHVGCESANTQVLQVSEACDAVFAVKESRGAR
 GVRVDFWRRRLRASLRLLTVWAPLLPLRIELTDTTLEQVRCWRVPGPAGCPAEPAEASDEAEERRARGCHLQYQR
 AGVRFAPFAAHPDGGRRLLTHLLGFDWLLDVSHLVAPHARVLDKRVASLESGRVVVGREPGVTSTIEVRSFLSD
 SILGEQALAVTDDKSVLELRLVQPVMGISLTLSRGTANFGEVTATPCWAQSALPAPKQEVALSILWLSFSDSTVAP
 AELVDRRDLGLSVSAEFPGATLEAEQQAQLGVVVSAGAGLPLHVALHPPEPCRRGRHRVPLASGTAWLGLP
 PASTPAPALPSSPAWSPATEATMGCKKQVAGSVGONTGVRGKFEKAEKARKEETEAREEEEEEEEMVPAFQ
 HVFELELGMVALLGVFCVAITFELVNGVVFVLRVYQKKEPPDSATDPTSPQPNWVWLGTQDELSKQLDRQSPG
 PPKGEGSCPCESGGGGEAPTLAPGFPGGTTSSSSTLARKEAGGRKRKRVFVTFVPAPPAQSFEEPVGAPAVQSI
 LVAGERDIRWVCEDMGLKDPLEELNYMERKINGSS

N-glycosylation site.

amino acids 106-109

Glycosaminoglycan attachment sites.

amino acids 480-483, 678-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 314-317

Tyrosine kinase phosphorylation site.

amino acids 758-766

N-myristoylation sites.amino acids 109-114, 111-116, 193-198, 397-402, 454-459, 472-477, 476-481,
 516-521, 550-555, 553-558, 672-677, 693-698, 694-694**Amidation sites.**

amino acids 312-315, 543-546, 706-711

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FIGURE 112

MATKTELSPATAKESKNAQDMQVDETLIPREGPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQS
 QLNDSSSEVLFEVDSFGGLSKAPKSLPAKSSILGGQFAIWEKRGPPQERSRLCSIALSGMLLGCFTAILIGGFISE
 TLGWFFVFYIFGGVGCVCCLLWFVVIYDDPFSSYPWISTSENEYIISLKKQVGSSEKQPLPIKAMLRSLPIWSIC
 LSCFSSQWLVSTMVVIYIPTYISSVYHVNTIRONGLLSALFFIVAWVIGMVGGYLADFLLTKKFRLITVRKIATIL
 GSLPSSALIVSLEYLNSGYITATALLTLSCGLSTLCQSGIYINVLDTAPRYSSFLMGASRGFSSTAPVIVPTVS
 GFLLSQDPFPGWRNVFFLLFAVNLLGLLEPYLIFGEADVQEWAKERKLTRL

Transmembrane domains.

amino acids 124-144, 154-174, 255-275, 287-307, 319-339, 350-370, 385-405

N-glycosylation sites.

amino acids 49-52, 60-63, 68-71, 77-80

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-418

N-myristoylation sites.

amino acids 106-111, 131-136, 135-140, 143-148, 160-165, 163-168, 255-260,
269-274, 272-277, 297-302, 335-340, 353-358

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FIGURE 113

MQVDETLIFRKVPSLCSARYGIALVLEFCNFTTIAQNVIMNITMVAHVNSTSPQSOLNDSSEVLFPVDSFGGLSK
APKSLPTKSSITLGGQFAIWEKNGFPQERSRLCSIALSGMLLGCFTALLIGGFTSETLGWFFVFYIFGGVGCVC
LLWFVVIYDDFVSYFWLSTSEKEYIISLKKQVRSNQFLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVIPT
YISSVYHVNIRONGLLSALPFIVAWVIGMVGGYLADFLITKKFRLITVRKIATILGSLPSSALIVSLPYLNSGY
ITATALETLSCGLSTLCQSGIYINVLDIAPRYSSFLWASRGFPSSIAPVIVPTVSGFLLSQDPEFGWRNVFFLL
FAVNLLGLLFYLIFFGEADVQEWAKERKITRL

Transmembrane domains.

amino acids 22-42, 105-125, 137-157, 236-256, 268-286, 300-320, 331-351,
366-386

N-glycosylation sites.

amino acids 30-33, 41-44, 49-52, 58-61

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 396-399

N-myristoylation sites.

amino acids 87-92, 112-117, 116-121, 124-129, 141-146, 144-149, 236-241,
250-255, 253-258, 278-283, 316-321, 334-339

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FIGURE 114

MAGAGPKRRRLAAPAAEEKEEAREKMLAAKSADGSAPAGEGEGVTLQRNITLLNGVALIVGTIIGSGIFVTPTG
VLKEAGSPGLALVWHAACGVFSTVGCALCYAELGTTISKSGGDYAYMLEVYGSFLPAFLKILWIELLIIRPSSQYIV
ALVPATYLLKELFPTCPVPEREAAKLVAACLCVLLLEAVNCYSVKAATKVDAPFAAAKLLALALITLLGQVQIGKG
DVGNLDEKPFSTFEGTKLDVGNIVLALYSGLFAYGGWNYINFEVTEEMINPYRNLPLAIIISLPVTLVYVLENLAY
FTTLSTRQMLSSRAVAVDFGNVHLGVMSWILPVFVGLSCFSGSVNGSLFTSSRLFFVGSREGHLPSILSMILPQL
LTPVPSELVFTCVMTLLYAFSKDIFSVINFFSFTNWLCVALAIIIGMIWLRHRKPELERPIKVNLAIPVFFILACL
ELIAYSPWKTFVECGIGFTIILSGLPVYFFGVWKNKPKWLLQGIFSTTVLCQKLMQVVPQET

Transmembrane domains.

amino acids 48-68, 83-103, 120-140, 137-157, 165-188, 200-220, 236-256,
274-294, 316-336, 364-384, 394-414, 430-450

N-glycosylation sites.

amino acids 49-52, 340-343

Tyrosine kinase phosphorylation site.

amino acids 112-119

N-myristoylation sites.

amino acids 34-39, 61-66, 107-112, 114-119, 125-130, 337-342, 341-346,
353-358, 459-464, 468-493

Amino acid permease.

amino acids 46-481

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FIGURE 115

MAGAGPKRRALAAPAAERKEEAREKMLAAKSADGSAPAGEGEGVTLQRNITLLNGVAITVGTITGSGIFVTFTG
VLKEAGSPGLALVWRAACGVFSIVGALCYAELGTTISKSGGDYAYMLEVYGSLEAFKLWTELLIIRPSSQYIV
ALVFATYLLKPLFPPTCPVPPEEAAKLVACLCLVLLLTAVNCYSVKAATRVQDAFAAAKLLALALIILLGFVQIGKG
DYSMLDPNFSFEGTKLDVGNITVLALYSGLFAYGGWNYLNFVTEEMINPYRNLPLAIIISLPITVLVYVLTNLAY
FTTLSTEQMLSSSEAVAVDFGNYHLGVMSWILPVFVGLSCFGSVNGSLFTSSRLFFVGSREGHLPSILSMINPQL
LTPVPSLVPTCVMTLLYAFSEKDTFSVINFFSFFNWLCVALAITGMWLRHRKPELEKPIKVNLALEVPFILACL
ELIAVSFWKTPVECGIGFTIILSGLPVYFFGVWKNKPKWLLQGIFSTTVLCQKLMQVVFQET

Transmembrane domains.

amino acids 48-68, 83-103, 120-140, 137-157, 165-185, 199-219, 236-256,
274-294, 316-336, 364-384, 394-414, 430-450

N-glycosylation sites.

amino acids 49-52, 230-233, 340-343

Tyrosine kinase phosphorylation site.

amino acids 112-119

N-myristoylation sites.

amino acids 34-39, 61-66, 107-112, 114-119, 125-130, 337-342, 341-346,
353-358, 459-464, 488-493

Amino acid permeases.

amino acids 46-481

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FIGURE 116

MALFTARPLLGSCTPALGSLLELLFSLGWVQPSRTLAGETGQEAAPLDGVLANPPNSSLSPRQLLGFPCEV
SELSTERVRELAVALAQKNVKLSTEQIRCLAHRLSEPPEDLDALPLDLLLFLNFOAFSGGEQACTREFFSRITKAN
VDLLPRGAPERQRLLEAALACWGVRSILSEADVRLSGGLACDLPGRFVAESAEEVLEPRIVSCTGFLLDQDQQA
ANAALQGGGFPYXGPPSTWSVSTMDALRGILLEVLGQPIIRSIPOGIVAANRQRSSRDPSWRQPERTILRPRFRE
VENTACPSGKKAREIDESLIFYKWELEACVDAALLATQMDRVNAIPFTYEQLVLLKHLDELTPQGYFESVIO
HIGYLFLLKMSPEDIPKWNVTISLETALKALLEVNKGHEMSPQVATLIDREVKRGQLDKDTLDTLTAFYFGLCSL
SPEELSSVPPSSIWAVEPQDLDTCPNQLEVLVYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSOQNVSM
DLATFMKLRDVAFLPTVAEVQKLLGPHVEGAKAEERHPPVRDWILRQRQDLDLGLGLQGGIPNGYLVLDLS
VQEALSSTPCLLGPFPVLTVLALLLASTLA

Signal sequence.

amino acids 1-33

Transmembrane domain.

amino acids 603-621

N-glycosylation sites.

amino acids 57-60, 388-391, 488-491, 515-518

Tyrosine kinase phosphorylation site.

amino acids 353-360, 471-477

N-myristoylation sites.amino acids 171-176, 174-179, 186-191, 266-271, 501-506, 577-582, 580-585,
581-586**Amidation site.**

amino acids 304-307

Leucine zipper pattern.

amino acids 101-122

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FIGURE 117

MALPTARPLLGSCTEALGSLFLFLFSLGWVQPSRTLAGETGQEAAPLDGVLANPFTNISSLSFQQLLGFPQAEV
SGLSTERYRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALFLDLLFLNFDAPSGFPQACTRFFSBITKAN
VDLLPRGAPERQRLPAAALACWGVVGSLLSEADVRAALGSLACDLPGRFVAESAELVLLPRLVSCFGFLDQDQQA
ARAALQGSGFPYGPSTMSVSTMDALRGLLFVLGQPIIRSIPOGIVAARQRSSRDPSWRQPERTILRPRFRE
VENTACPSGEEKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPGGYFESVIQ
HLGYLFLKMSFEDIKKNVTSLETILKALLEVNKGHEMSPOVATLIDRFVNGRGQLDKDTLDTLTAIFYPGYLCSL
SPEELSSVFPSSIWAVRPQDLDTCDPRQLDVLVPHARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSOQNVSM
DLATFMKLRDVAFLFLVAEVQKLLGPHVEGLKAREERNRPVBDWILRQRQDULDTLGLGLQGGIFNGYLVLDLS
VQEALSGTPCLLGGPGPVLTVLALLASTLA

Signal sequence.

amino acids 1-33

Transmembrane domain.

amino acids 603-621

N-glycosylation sites.

amino acids 57-60, 388-391, 488-491, 515-518

Tyrosine kinase phosphorylation sites.

amino acids 353-360, 471-477

N-myristoylation sites.amino acids 171-176, 174-179, 186-191, 266-271, 501-506, 577-582, 580-585,
581-586**Amidation site.**

amino acids 304-307

Leucine zipper pattern.

amino acids 101-122

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FIGURE 118

MATTVPDGGCRNGLRGEYKRLCDKAEANGIVLETVATAGVVTSAFMTLPILVCKVQDSNDRGMLPTQFLFLIG
VLGIFGLTFAFIIGLDGSTGPTTRFTLFGILFSICFSCILAHAVSETKLVRGRKPLSLLVTILGLAVGFSLVQDVI
AIEYIVLTMRRTNVNVFSELSAPRRNEDFVLLTTYVLFMLALTFLMSSFTFCGSFTGWKRKGASHIYLTMLLSIA
IHWAVITLLMLPDDFDRWDDFILSSALAANGWVFLAYVSPEFWLLTKQRNPMDYPVEDAFCKPQLVKKSYGVE
NRAYSQEEITQGFEETGDTLYAPYSTHFQLQNQPFQKEFSIPRAHAWPSFYKDYEVKKEGS

Transmembrane domains.

amino acids 30-50, 66-86, 98-118, 121-141, 137-157, 174-194, 212-232, 244-264

N-glycosylation site.

amino acids 158-161

N-myristoylation sites.

amino acids 8-13, 38-43, 80-85, 88-93, 102-107, 136-141, 201-206

Amidation site.

amino acids 124-127

7 transmembrane receptor.

amino acids 27-273

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FIGURE 119

MIPFLPMFSLMLLLIVNPFINANNHYDKILARSRIQRDQGFNVCAQQILGTNNKYFSTCKNWKYSICGQKTT
 VLYECCPGYMRMEGMKGCPAVLFDHVGTLGIVGATTTQRYSDASKLREEIEGKGSFTTYFAFSNEAWDNLDSD
 IRRGLESNVNVVELLNALESHMINERMLTSDLNKNGMITPSMYNNLGLFINHYFNGVVTVMNCARIHGNQIATNGV
 VHVIDRVLTQIGTSTQDFIEARDDLSFPRAAITSIDLEALGRDGHFTLFAPTNEAFKELPRGVLERFMGDKVA
 SEALMKYHTINTLQCSSESIMGGAVFETLEGNTIEIGCDGDSITVNGIKMVNKKDIVTNNGVIHLIDQVLPDGA
 KQVIELAGKQOTTFTDLVAQLGLASALRPDGEYTLAPVNNAFSDDTLSMVQKLLKLILQNHILKVKVLNELY
 NGQILETIGGKQLRVFVYRTAVCIENSCMEKGSFQGRNGAINTFREIIFPAEKSLREKLKQDKRFSTFLSLLEA
 ADLKELLTQPGDWTLFVFTNDAPKGMTSEKELLIRDKNALQNLILYHLTFGVFIGKGFEPGVTNILKFTTQGSK
 IFLKEVNDTLLVNELKSKESDIMITNGVIRHVVDKILYPADTPVENDQLEILNKLTIKYIQIKFVRGSTEKEIFV
 TVYTTKLITKVVEPKIKVIEGSLQPIIKTEGPTLTKVKIEGEPFRLIKEGETITEVINGEPIIKKYTKLIDSV
 PVEITEKETREERIITGPEIKYTRISTGGETEETLKKILLQREVTKVTKFIEGGDGHLPEDBEIKRLLQGUTPV
 RKLQANKKVQSSRRRLREGRSQ

Signal sequence.

amino acids 1-21

N-glycosylation site.

amino acids 599-602

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 507-510, 731-734

N-myristoylation sites.

amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,
476-481, 570-575, 768-773

Fasciclin domain.

amino acids 94-232, 496-630

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FIGURE 120

MIPFLPMFSLLLLLIVNFINANNHYDSTLARSRIGRDQGENVCALQQILGPKKKYFSTCKNWKYSICGQKTT
 VLYECCPGYMPMEGMEKGPVAVLPIDHVGTLGIVGATTTQRYSDASKLREEIRGKGSFTYFAPSNESAWNLDSD
 IRRGLESNVNVVELLNALBSHMINKRMLTKDLKNGMIIFSMYNNLGLFINHYPNGVVTVNCARITHGNQIATNGV
 VHVIDRVLTOIGTSTIQDFIEAEDDLSSFRAAAITSDILEALGRDGHFTLFAPTNEAFEKLPFGVLERINGDKVA
 SEALMKYHIINTLQCSSESIMGCAVFETLEGNTIIEIGCDGDSITVNGIKMVNKKDIVTNMGVIHLTUQVLIPOSA
 EQVIELAGKQOTTTFTDLVAQLGLASALRPDGEYTLAPVKNAPSDDTLSMDQRLKLILQNHILKVKVGLNELY
 NQQILETIGSKQLRVFVYRTAVCTIENSCMEKSGSKQGRNGATHIFRETIINPAEKSLNEKIKQDKRFSTFLSLLEA
 ADLKELLTQPGDWTLFVPTNDAFKGMTSEEKEILIRDKNALQNIILYHLTPGVFLGKGFEFGVTNLIKTTQSSK
 IFLKEVNDTLLVNELESKESQIMTTNGVIEVVDKLLYPADTPVGNDQLEILNKLIKYTIQTFVRGSTFKEIFV
 TVYRPTLTQVKLEGEPEFRLIKEGETITEVIHGEPTIKKYTKIIDGVFVEITEKETREERIITGPRIKYTRIST
 GGGETEETLKNLLQSEVTRVTKFIEGGDGHLEFEDEEIKRLIQGDTPVRKLQANKKVQGSRRRLRGRSQ

Signal sequence.

amino acids 1-21

N-glycosylation site.

amino acids 599-602

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 507-510, 704-707

N-myristoylation sites.

amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,
476-481, 570-575, 741-746

Fasciclin domains.

amino acids 94-232, 234-367, 370-494, 496-630

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FIGURE 121

MIFPLEMFSLLMLLVNPFINANNHYDKILANSRIRGRDQGFNVCALQQILGTKKKYFSTCKNWKYSICGQKTF
 VLYECCPGYMRMEGMEKGCFAVLPTDHYVGTGIVGATTTQRYSDASKLREEIEGKGSFTTYFAPSNEANDNLDSQ
 IRRGLESNVINVELLINALHSHMINKPMLTKDLKNGMIIPSMYNNLGLFINHPNGVVTVMNCARITHGNQIATNGV
 VHVIDRVLTQIGVSTIGQFTEAEDDLSSFRABAITSDILEALGRDGHFTLFAPTNEAFKLPFGVLERIMGDKVA
 SEALMKYHILNTLQCSSEIMGGAVFETLEGNTIEIGCDGDSITVNGIKMVNKKDVTNNGVIELTDQVLPDSA
 KQVIELAGKQOTTFTDLVAQLGLASALRPDGEYTLAPVNNAFSDDTLSDQRLKILQNHILKVKVGLNELY
 NGQILETIGGKQLRVFVYPTAVCIENSCMEKGSQGRNGAIHITRETIKPAERSLHEKCLKQDKRFSTFLSLLEA
 ADLKELLTQPGDWTFLFVPTNDAFKGMTSEEKELLIRDKNALQNIILYHLTPGVFICKGFEPCGVNIIKTTQGSK
 TFLKEVNDTLLVNELKSKESDIMTTNGVIRVVDKLLYPADTPVGNQDQLEILNKLKIKYIQIKFVRGSTEKEIFV
 TVYKPIIKKYTKIIDGVFVSEITEKETREERTITGPEIKYTRISTGGGETEETLKKILQEDTPVRKLQANKKVQG
 SPRRLKEGRSQ

Signal sequence.

amino acids 1-21

N-glycosylation site.

amino acids 599-602

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 507-510, 674-677

N-myristoylation sites.

amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,
476-481, 570-575, 711-716

Fasciclin domains.

amino acids 94-232, 234-367, 370-494, 496-630

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FIGURE 122

MIPFLPMFSLLLLLLIVNPFINANNHYKILAHSKIRGRDQGFNVCAQQILGTFKKKYPSTCKNWKYSICGQMTT
 VLYECCPGYMRMEGKGCFAVLFDHVGTLGIVGATTTQRYSDASKLREELRGKGSFTYFAPSNEAWDNLOSD
 TRRGLESNVNVELLNALASHMINKFMLETKDLKNGMIIPSMYNNLGLFTNHYPNGVVTVNCARTINGNQIATNGV
 VHVIDRVLTQIGTSIQDFIEAEDDLSSFRAAAITSDILEALGRDGHFTLFAPTNEAFEKLPFGVLERIMGDKVA
 SEALMKYHILNLTQCSSEIMGGAVFETLEGNTIEIGCDGDSITVNGIKMVNKKDIVTNNGVINHLDQVLIPOSA
 KQVIELAGKQQTTFDILVAQLGLASAIRPDGEYTLAPVWNAFSDDTLSMDQRLKLILQNHILKVKGVLNELY
 NGQILETIGGKQLRVFVYRTAVCIENSCHEKGSKQCGNGAIHTFRETIKFAEKSLHEKLGKQKREFTFLSLEA
 ADLKELLTQPCDWTLPVFTNDAFKGMTSEEKEILIRDKNALQNIILYHLTPGVFLGKGFEPGVTNILKTTQGSK
 IFILKEVNDTLLVNELKSKESDIMTTNGVIEHVVDKLLYPADTFVENDQLEILNKLIKYTIQIKFVRGSTFEKIFV
 FVYRPTLTKVKIEGEPFRLINEGETITEVINGEPIIKKYTKIIDGVFVEITEKETREERRIITGPEIKYTRIST
 GCGETEETLKKLLQEDTFVRKLQANKKVQGSRRRLREGRSQ

Signal sequence.

amino acids 1-21

N-glycosylation sites.

amino acids 599-602

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 507-510, 704-707

N-myristoylation sites.

amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,
476-481, 570-575, 741-746

Fasciclin domains.

amino acids 94-232, 234-367, 370-494, 496-630

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FIGURE 123

MIPFLPMFSLLLLLLVNPNAMNHDKILAHSRIRGRDQSPNVCAQQILGTKKKYPSTCKNWWYKKSICGQKTF
 VLYECCPGYMRMEGMKGCFAVLPIDHVYGTLSIVGATTTQRYSDASKLBEEIEGEGSTTYFAPSNEAWDNLDSD
 IRRGLESNVNVVELLNALSHMINKRMLTKDLRNGMIIPSMYNNLGLFINHYFNGVVTVNCARTIHGNQIATNGV
 VHVIDRVLTQIGTSTIQDFIEAEDDLSSFRAAAITSDIIEALGRDGHFTLFAPTNEAFKELFRGVLERIMGDKVA
 SEALMKYHIILNTLQCSSEIMGGAVFTLEGTITIEIGCDGDSITVNGIKMVNKKDIVTNNGVTHLIDQVLIPDSA
 KQVIELAGKQQTTFYDLVAQLGLASALRPDGEYTLAPVNNAFSDUTLSMDQRLKLLQNHILKVKVLNELY
 NGQILETIGGKQLFVVFYRTAVCIENSCMEKSGSKQGRNGCAIHIFREIIKPAEKSLERKQDKKPFSTFLSLLEA
 ADLKELLTQPGDWTFLVPTNDAFKGWTSEKELLIRDKNALQNTILYHLTFGVFIGKGFEPGVNLIKTTQGSK
 IFLKEVNDTLLVNELEKSKESDINTFNGSVIHVVDKLLYPADTFVGNLQLEILNKLINIKYIQIKFVNGSTFKETPV
 TVYKPIIKKYTKIIDGVFVEITPEKETREERIITGPETKYTRISTGGGETEETLKKLLQEEVTKVPKFIEGGDGH
 LFEDEETIKRLQGDTPVRKLQANKKVQGSRRRLREGRSQ

Signal sequence.

amino acids 1-21

N-glycosylation site.

amino acids 599-602

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 507-510, 674-677

N-myristoylation sites.

amino acids 70-75, 106-111, 109-114, 192-197, 193-198, 214-219, 392-397,
476-481, 570-575, 711-716

Fasciclin domains.

amino acids 94-232, 234-367, 370-494, 496-630

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FIGURE 124

MVNYAWAGRSQRKLLWRRSVAVLTCKSVVRPGYRGGLQARRSTLLKTCARARATAPGAMKMVAPWTRPFYSHSCCL
CCHVRETGITILLGVWYLIINAVVILLILLSALADPDQYNFSSSELGGDFEFMDANMCIATAISLLMILICAMATY
GAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPNSTQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISII
LTFKGYLISCWNCYRYINGRNSSDVLVYVTENDTTVLLFPYDDATVNGAAKEPEPEFYVSA

Transmembrane domains.

amino acids 83-103, 124-144, 162-182, 205-225

N-glycosylation sites.

amino acids 111-114, 244-227, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 39-42

Tyrosine kinase phosphorylation site.

amino acids 243-251

N-myristoylation site.

amino acids 34-39

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FIGURE 125

MPGQGGGLQARRSTLLKTCARARATAPGAMEMVAPWTRFYSNSCCICCHVRTGTILLGVWYLIINAVVLLILLSA
LADFDQYNFSSSELGGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWLI PFFCYQLFDFALNMLVAI
TVLIYPNSIQBYIRQLPPNFFPYRGGVMSVNPTCLVLIILLFISILLTFKGYLISGVWNCYRYINGRNSSDVLVY
VTSNUTTVLLFPYDDATVNGRAKEFFPPFYVSA

Transmembrane domains.

amino acids 54-74, 95-115, 133-153, 176-196

N-glycosylation sites.

amino acids 82-85, 215-218, 226-229

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 10-13

Tyrosine kinase phosphorylation site.

amino acids 214-222

N-myristoylation site.

amino acids 5-10

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FIGURE 126

MGRAGGGGPGRGPPPLLLFLGAALVLASGAVFAREAGSRVEAEELVKGSFAWEPPANDTRERAGPPAAGEDEAS
WTFAGGELAGPHEVLQESAAVTGTAWLEADSPGLGGVTAEAGSGDAQALPATLQAPHEVLGQSIMPFAIPRATE
ASGPPSPPTPGDKLSPASELPKESFLEVWLKLGGSPTDPQVPELTYPFGSTLEPQPASDITDIDYFESLDGEGNG
ADLGSFPGSPGTSENHPDTEGHTPSWSLLDLYDDFTPFDESDFYPTTSFYDDLDEEEEEEDDKDAVGGGULED
EMELLVPTGKPGIGPCTGQETSRKHA VFPQHTLGSSVPSSSIALRPRPGEPGRDLASSENGTECRSGFVRHNGSC
RSVCDLFPSYCHNGGQCYLVENIGAFRCRCNTQDIYWHKGMRCESIITDFQVMCVAVGSAALVLLLLFMMTVFFA
KKLYILLKTENPKLARTNKERTPSELANDNFSLSLIAEGSHFNDDPSAPHKIQEVLSCLKEESFNQNSMSFK
LEGKGEDQADLDVNCIQMMLT

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 423-443

N-glycosylation sites.

amino acids 57-60, 355-358, 367-370, 473-476

N-myristoylation sites.amino acids 6-11, 29-34, 79-84, 109-114, 116-121, 222-227, 226-231, 230-235,
233-238, 308-313, 314-319, 330-338, 334-339, 368-373, 482-487

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FIGURE 127

MLPVYQSEVKPNPLQDANICSRVFFWNLMELFKIGHKRRRLREDDMYSVLPEDEPSQHLGEELQGFWDKEVLRAND
 AQKPSLTRAIIKCYKWSYLVLSGIFTLIERSAKVIQPIFLGKIINYFENYDPMDSVALNTAYAYATVLTFFCTLIL
 AILSHLYFFYHVQCAGMRLRVAMCHMIYRKALRLSNMAMGKTTTGGQIVNLLSNDVNKFDQVTVFLHFLWAGFLQA
 LAVTALLMMREICTSCLAGMAVLIILLFLQSCFGKLFSSLRSEKTATFTDARIRTMNEVITGIRLIKMYAWKESFS
 NLITNLRKKEISKILRSSCLRGMNLASFFSASKIIVFVTFVTFFVLLGSGVITASRVFVAVTLYGAVKLTVTLFFF
 SAIERVSEATVSLRIQTFLLLDEISQRNKLPSDGKKMVMHVQDFTAFWDKASETFTLQGLSFTVRPGELLAVV
 GPVCGAGKSSLLSAVLGRLAPSHGLVSVHGRVIAVVSQGPWFVPSGTLRSNILFGKKYEKERYEKVIKACALKKDLO
 ILLEDGDLTVIGDRGTTLSGGQKARVNLARAVYQDADIYLLDDPLSAVDAEVSRLHFELCICQILHEKITILVTH
 QLQYLKAASQILILKDGKVMQKCTYTEFLKSGIDFGSLLKKONEESEQPPVFGTETLRNKEFFSESSVNSQQSSR
 PSLRDLGALESQDTENVPTLSEENRSECKVGTQAYKNYFRAGAHWIVFTPLILINTAAQVAVYLQDWWLSYWAN
 KQSMNLNVTNCGGNVTEKLDLNLWYLGIYSGLTVATVFLGRIARSLLVFYVLNSSQTLNKKMFESILKAPVLFED
 RNPIGRILNRFSKDIGHLDLLEFLTFDQFIQTLLQVVGVSVAVAVIPWIAIPLVPLGIIFFILRRYFLETSRD
 VKRLESTTRSPVFSRLSSSLQGLWTIRAYKAEKQCQELFDAHQDLRGEANFLFLTTSRWFAVRLEAICAMFVII
 VAFGSLILAKTLUAGQVGLALSYALFLMGFMQCVROSAEVENMMISVERVIEYTOLEKEAFWEYQKRPPFAWF
 HEGVILFDNVNFMYSFGGELVLRRLTALIKSQEKVQIVGRTGAGKSSLLSALFRLSEFECKIWKILTTEIGL
 HDLRKKMSTIPQRPVLFSTMRKNLDPFKENTDEELMNALQEVQLKETIEDLPCKMUTELAESGSNFSVQGPQL
 VCLARAILRKNQILIIDEATANVDPRTELIQKKIREKFAHCTVLTIAHRLNTIIDSOKIMVLDSGRLEKEYDEF
 YVLLQNKESLFYKMNQQLGKAEAAALTETAKQVYFKNYPHIGHTDHMTNTSNCQPSLTITIFETAL

Transmembrane domains:

amino acids 134-154, 233-253, 346-366, 708-728, 767-787, 834-854, 857-877,
 948-968, 987-987

N-glycosylation sites.

amino acids 651-654, 690-693, 746-749, 754-757, 792-795, 1176-1179, 1309-1312

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 1115-1118

Tyrosine kinase phosphorylation sites.

amino acids 37-45, 497-504, 1253-1259

N-myristoylation sites.

amino acids 192-197, 310-323, 343-348, 430-435, 448-453, 487-492, 532-537,
 537-542, 624-629, 672-677, 752-755, 766-771, 770-775, 779-784, 980-985,
 1078-1083, 1174-1179, 1313-1318

Amidation sites.

amino acids 405-410, 495-500

ATP/GTP-binding site motif A (P-loop).

amino acids 445-452, 1075-1082

ABC transporter.

amino acids 438-509, 1068-1250

ABC transporter transmembrane region.

amino acids 92-365, 711-997

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FIGURE 128

MSALRRRTFGDDYQVVTTSSSGSLQFQGFQGFQFQQQLVPKKKQRFFVDKNGRCNVQSGNLGSETSRYLSDLFTF
LVDLKWRWNLFIFILPYTVAWLFMASMWWVIAVTRGDINKAHVGNVTPCVANVYNFSAFLFFIETETIGXGY
RYITDKCFEGYLLFLFQSIILGSTVDAFLIGCMFIKMSQPKKRAETLMFSEHAVISMRDGLTLMFRVGNLRNSH
MVSAGIQCILLKSRQTPEGEFLFLDQLELDVGFSTGADQLFLVSELTICHVIDAKSPFYDLSQRSMQTEQFEIV
VILEGIVETTGMTQARTSYTEDEVWGHRRFFVISLEEGFTKVOYSQPHATFEVPTPPYSVKEQEEMLLMSSP
LIAFAITNSKERHNSVECLDGLDITTTKLPSKLQKITGREDFPKLLRMSSTTSEKAYSLGDLNKLQRISSVP
GNSEKLVSKTTKMLSDPMSQSVADLFPKLQKMAGGAARMEGNLPAKLKMNISDRFT

Transmembrane domains.

amino acids 83-103, 120-140, 158-178

Glycosaminoglycan attachment site.

amino acids 20-23

N-myristoylation sites.

amino acids 58-63, 61-66, 216-221, 301-306, 486-491

Cell attachment sequence.

amino acids 109-114

Inward rectifier potassium channel.

amino acids 47-393

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FIGURE 129

MPLEFKNTSVSSSLYSGCRLTLLRPEKDGAAATRVDAVCTHRPDPKSPGLDRERLYWNLSQLTHGITELGPHYTLDRH
 SLVYNGFTHQSSMTTTRTFDTSTMHLATSRTPEASLSGPTTASPLLVLTINFTITNLRYEENMMHHPGSRKFNTT
 ERVLQGLLRPFVFKNTSVGPLYSGCRLTLLRPEKDGAAATKVDAICTYRFPDPKSPGLDREQLYWELSQLTHSITEI
 GPYTLDRDSLTVNGFTQSSSVPTTSIPGTFPTVDLGTSGTFVSKPGPSAASPLLVLTINFTITNLRYEENMQHF
 GSRKFNTTERTVLQGLLRSLFKSTSVGPLYSGCRLTLLRPEKDGATGVDICTHSPDPKSPRLDREQLYWELSQL
 LTHNITELGHYALDNDSELFVNGFTHRSSVSTTSTPGTFPTVYLGAASKTEASTEGPSAASHLLILFTLNFTITNLR
 YEENMWPGSRKFNTTERTVLQGLLRPLFKNTSVGPLYSGSRLTLLRPEKDGATGVDICTHRPDPTGPGLDREQ
 LYLELSQLTHSITELGPHYTLDRDSLTVNGFTHKSSVPTTSTGTVVSEEPFTLNFTINNLRYMADMGQFGSLNFTI
 TDNVMKHLSPFQSSSIGARYTSCRVIALLRSVKNGAETRVDLLCTYLQPLSGGGLPIKQVFHLSQQTHGITH
 LGPYSLDKDSLTVNGYNEFGLEPPTTPKPAFTFLPPLSEATTAMGYHLEKTIITLNFTITNLRYMADMGQFGSATF
 NSTEGLVQLHLLRPLFQKSSMGPFYLGCCQLISLRPEKDGAAATGVDTTCTYRFPDPVPGGLDIQQLYWELSQLTHGV
 TQLGFYVLDROSLFINGYAPQNLIRGEYQINFHIVNWNLSNPDPTSSHYITLLRDIQDEVTTLYXGSQLHDTF
 RFCLVTNLTMDSVIVTVKALFSSNLDPSLVEQVFLDKTLNASFWLGSYQLVDIHVTEMESSVYQPTSSSSSTQ
 HFYPNFTITNLPSYQDKAQFPTTNYQRNKNIEDALNQLFRNSSIKSYFSDCCQVSTFRSVFNRRHTGVDSLCNF
 SPLARRVDRVAIYEEFLEMTRNGTQLQNFITLDRSSVLVDGYSPNRNEPLTGNADLPFWAVIFIGLAGLLGLITC
 LICEVLVTTTRRRKKKESEYNVQQQCPGYQSHLEEDLQ

Transmembrane domains.

amino acids 107-127, 418-438, 1093-1113

N-glycosylation sites.

amino acids 6-9, 125-128, 146-149, 162-165, 281-284, 302-305, 374-377,
 385-388, 437-440, 457-460, 473-476, 570-573, 591-594, 721-724, 741-744,
 836-839, 853-856, 895-898, 923-931, 967-970, 1004-1007, 1058-1061, 1064-1067

Glycosaminoglycan attachment site.

amino acids 644-647

Tyrosine kinase phosphorylation sites.

amino acids 358-365, 1121-1128

N-myristoylation sites.

amino acids 15-20, 171-176, 260-265, 310-315, 327-332, 339-344, 482-487,
 583-588, 611-616, 778-783, 782-787, 1106-1111, 1114-1119

SEA domain.

amino acids 112-245, 270-391, 661-684

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FIGURE 130

MGNWVNVNHWESVLFVFLVWGLNVFLFVDAFLKYEKADKYYYYTRKILGSTIACARASALCLNFNSTLILLEFVCRN
LLSFLRGTCSEKFLAKQLDHNLTFFHKLVAYMICLHTAIHIIAHLFNEDCYKSRQATDQSLASILSSLSHDE
KKGGSWLNPIQSRNTTVEYVTFSTVAGLTGVIMTIALILMVTSADEFIRRSYFVFWYTHHLFIIFYILGLGING
IGGIVRGQTSESMNESHPRKCAESFEMWDDRDSDHCRPPKFEHGHPPEKWKILAPVILYICERILRFYRSQQKVV
ITKVVMBESKVLQLQMNKRGFSMEVGQYTFVNCPSISILEWHFPFTLTSAFEEDEFFSIHIFAAGDWTENLIRAFE
QQYSPIPRIEVDGPFGTASEDVFOYEVAVLVGAGIGVTPFASILKSIWYKFTQCADHNLKTKKLYFYWICRETGA
FSWFNNLLTSLEQEMSELGKVGFLNYRFLFTGWDSNIVGHAALNFDKATDIVTGLKQKTSFGGRPMWDMFSTIA
TSHPKSVVGVFLCGPRFLAKSLRKCCCHRYSSLOPRKVQPYFNKENF

Signal sequence.

amino acids 1-29

Transmembrane domain.

amino acids 44-64, 60-80, 99-119, 168-188, 204-224

N-glycosylation sites.

amino acids 63-66, 97-100, 162-165, 236-239

Tyrosine kinase phosphorylation sites.

amino acids 198-206, 367-373

N-myristoylation sites.

amino acids 47-52, 135-140, 178-183, 225-230, 402-407, 527-532

Ferric reductase like.

amino acids 46-563

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FIGURE 131

MGNWVNVNHWFSVLFLVVLGLNVFLFVDAFLKYEKADKYYYTRKILGSTLACARASALCLNFNSTLILLPVCRN
LLSFLRGTCSPCSRTRLRKQLDHNLTTHKLVAYMICLWTAHTTAHLENFDCYSRSRQATDGSILSLSSLSHDE
KKGGSWLNPIQSRNTTVEYVTFSTIAGLTGVIMTIALILMVTSAFIFIRRSYFEVFWYTHLFTIFYILGLGING
EGGTIVRGQTTEESMESHPRKCAESFENWDDDRDSHCRPKFEGHPPESWKNILAPVILYICERILRFYRSQQKV
ITKVVMHPSKVLLELQMNKRGFSMEVGYTFVNCPSISLLEWHPPFTLTSAPTEEDFTSIHTRAAGDWTENLIRAF
QQYSPPIPRLEVDGPFCTASEDVFQYEVAVLVGAGIGVTPFASILKSIWYKFCADHNLRTKSIYFYWICKETGA
FSWFFNLLTSLQEMEELGKVGFLNYFLFLTGWDSNIVGHAALNFDKATDITGLKQKTSFGRPMWDNEFTIA
TSHPKSVVGVFLOGPRTLAKSLRKCHRYSSLDPRKVQFYFNKENF

Transmembrane domains.

amino acids 6-26, 44-64, 60-80, 99-119, 168-189, 204-224

N-glycosylation sites.

amino acids 63-66, 97-100, 162-165, 236-239

Tyrosine kinase phosphorylation sites.

amino acids 198-206, 367-373

N-myristoylation sites.

amino acids 47-52, 135-140, 178-183, 225-230, 402-407, 527-532

Ferric reductase like transmembrane.

amino acids 46-563

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FIGURE 132

MGNWVYNHWFSVLFVVLGSLNVFLFVDAFLKYEKADKYYYYTRKILGSWKWILAPVILYICERTILRFYRSQQKV
VITKVVMHPSKVLELQMNKRGFSMEVGGYIFVNCFSISLLEWHFFETTSAPERDFFSLHIRAAGDWTENLIRAF
EQQYSPIPRIEVDGPFCTASEDVFOYEVAVLVGAGIGVTPFASILKSIWYKFQCADHNLKTKKVGHAALNFDKA
TDIVTGLKQKTSFGRFMWDNEFSTIATSHPKSVVGVFDCGERTLAKSLRKCCHRYSSLDPKVKQFYFNKENFO

Transmembrane domains.

amino acids 6-26, 44-64

Tyrosine kinase phosphorylation site.

amino acids 146-152

N-myristoylation sites.

amino acids 181-186, 257-262

Ferric reductase like transmembrane.

amino acids 1-293

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FIGURE 133

MGNWVYNHWFSLVFLVVMVGLVFLFVDAFLKYERADRYYYTRKILGSTLACARASALCLNFRSTLILLPVCRN
LLSFLRGTCSTFCSTLRKQLDHNLTFSKLVAYMICLHTAIHIIAHLFNEDCYSRSRQATDGLASILSSLSHDE
KKGGSWLNPIQSRNTTVEYVTFTSIAGLTGVIMTIALILMVTSAFIRKSYFEVFWYTHNLTFTFYILGLGIRG
IGGIVRGQTEESMNEESHPRKCAESFEMWDDRDSDHCRPRKFEGHPPESWNEWILAFVILYICERILRFYRSQQKV
ITKVVMHPSKVLLELQMNKRGFSMEVGCYIFVNCPSISLLEWHPTLTSAPEEDFFSIHIRAAGDWTENLIRAFE
QQYSFIPRIEVDGFFGTASEDVFQYEVAVLVGAGIGVTPFASILKSIWYKFCADHNLKTKKVGHAAALNFDKAT
DIVTGLKQKTSFGRPMWDNEFSTIATSHPKSVVGVFLCGPRTLAKSLRKCCCHRYSSLDPRKVQFYFNKENF

Transmembrane domains.

amino acids 6-26, 44-64, 60-90, 99-119, 169-188, 204-224

N-glycosylation sites.

amino acids 63-66, 97-100, 162-165, 236-239

Tyrosine kinase phosphorylation sites.

amino acids 198-206, 367-373

N-myristoylation sites.

amino acids 47-52, 135-140, 179-183, 225-230, 402-407, 479-493

Ferric reductase like transmembrane.

amino acids 46-514

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FIGURE 134

MTSGSVFFYILIFGKYFSHGGCQDVKCSLGYFPCGNITKCLFQLLHCGVDDCGNQADEDCGDNNGWSMQFDK
 YFASYYKMTISQYPFEAETPECLVGSVPVQCCLQGLELDCDETNLRAVPSVSSNVTAMSLQWNLIKLPDPCFKN
 YHDLQKLYLQNNKITSISTYAFRGINSITKLYLSHNPITFLKPGVFEDLHRLEWLIIEEDNHLNRISPTTFYGLN
 SLILLVLMNNVLTSLPDKPLCQHMPRLHWLDLEGNHINLRNLTFFISCSNLTVLVMRKNKINKHNENTTAPLQK
 LDELGLGSKNIENLPFLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKIKLSLSLEGIEISNIQQRMFPLMNL
 HIYFKKQYCYGYPHVRSCPKNTDGISSLENLLASIIQRVFWVVSVAVTFCFNI FVICMRPYIRSENKLYAMSI
 ISLCCADCLMGIYLFVIGSFDLKFGEYNKHAQLWMESTHCQLVGSLLAILSTEVSVLLLTFLTLEKYICIVYFF
 RCVRPEKCRITITVLILIWITGFIVAFIPLSNKEFFKNYYGTNGVCFPLHSEDTESIGAQIYSVAIFLGINIAAF
 IIVFSYGSMPFYEVSQSAITATEIRNQVKKEMILAKRFFIFVFTDALCWIFIFVVKFLSLLQVEIPGTITSWVV
 IFILPINSALNPILYTLTTRPPKEMIHREWYNYRQRKSMDSKQKTYAPSFIVVEMWPLQEMFPELKNFULTY
 PCEMSLISQSTRLNSYS

Transmembrane domains.

amino acids 212-232, 404-424, 443-463, 489-509, 526-546, 577-597, 629-649,
 665-685

N-glycosylation sites.

amino acids 36-39, 127-130, 264-267, 272-275, 329-328, 368-371

N-myristoylation sites.

amino acids 49-54, 352-357, 586-591, 659-664

Leucine zipper pattern.

amino acids 487-508

LDL-receptor class A.

amino acids 40-59

G-protein coupled receptor.

amino acids 159-189, 413-432, 422-452, 436-466, 478-518, 528-547, 625-644,
 673-689

Leucine rich repeats.

amino acids 127-150, 151-174, 175-198, 199-222, 223-246, 248-271, 272-295,
 296-319, 320-343, 344-367

7 transmembrane receptor (rhodopsin family proteins).

amino acids 485-681

Low-density lipoprotein receptor domain.

amino acids 25-64

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FIGURE 135

MTSGSVFFYILIFGKYPSRGGGQDVKCSLGYFPCGNITKCLPQLLHCNGVDDCCNQADEDNQGDNNGWSLQFDK
 YFASYKMTSQYFFEAEETFECLVGSVPVQCLCQGLELDCDETNLBAVPSVSSNVTAMSLQWNLIKLPDFCFKN
 YHDLQKLYLQNNKITSISIIYAFRCGLNSLTCLYLSNNRITFLKPGVFEDLHRLEWLTIEDNNLSRISPTTFYGLN
 SLILLVLMNNVLTFLPDKPLCQMMERLHWLDLEGNNHNNLRNLTFISCSNLTFLVMKRNKINHLNENTTFAPLQK
 LDELGLGSNNKTIENLPFLIFKDLKELSQLNLSYNPIQKIQANQFDYLVKLSLSLEGIEISNIQORMFRPLMNL
 HIYFKKFQYCGYAPHVRSCKENTDGISSLENLLASIIQRFVFWVVSVAVTCFGNIFVICMRPIIRSENKLYAMSI
 ISLCCADCLMGIYLFVIGGFDLKFRGEYNKHAQLWMESTHCQLVGSLLALLSTEVSVLLLTFLTLEKYICIVYRF
 BCVRPFGKCRITITVLLILIWITGEIVAFIPLSNKEFFKNYYGTNGVCFPLESEDTESIGAQIYSVAIFLGINLAA
 ITIVFSYSGSMFYSVNSAITATEIRNQVKEMILAKNEFFIVFTDALCWIPFVVKFSLQLQVEITPGTITSWV
 IFILPINSALNFIPLYTLTTFPKEMIRFWNYRQRKSMDSKGQKTYAPSFIVVEMWPLQRMPPFLMKPDFTY
 PCMSLISQSTRSNSYS

Transmembrane domains.

amino acids 212-232, 404-424, 443-463, 489-509, 526-546, 577-597, 629-649,
 665-685

N-glycosylation sites.

amino acids 36-39, 127-130, 264-267, 272-275, 325-328, 368-371

N-myristoylation sites.

amino acids 49-54, 352-357, 586-591, 659-664

Leucine zipper pattern.

amino acids 487-508

Leucine rich repeats.

amino acids 127-150, 151-174, 175-198, 199-222, 223-246, 248-271, 272-295,
 296-319, 320-343, 344-367

7 transmembrane receptor (rhodopsin family).

amino acids 59-259

Low-density lipoprotein receptor domain.

amino acids 25-64

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FIGURE 136

MGRLASRPLLLALLSLALCRGRVVRVPTATLVRVVGTELVIPCNVSDYDGPSEQNFQNSFSSSLGSSFVELASTW
 EVGFPAQLYQERLQGEILLARTANDAVELRLKNVQPSDQGHYKCSTPSTDATVQGNIEDTVQVKVLADSLHVG
 PSARPPPSLSLREGEFFELRCTAASASELHHLALLWEVHRGPARDSVLALTHEGRFHPGLGYEQRYHSGDVRL
 DTVGSDAYRLSVSRALSADQGSYACIVSEWIAEQGNWQEIQEKAVEVATVVVIQPTVLRAAVPRNVSVASGKELD
 LTCNITTDKADDDRPEVTFWTFSRMPDSTLPGRSVLARLDKSLVHSSPVALSHVDARGYHLLVRDVSKEKNSGY
 YYCHVSLWAPGHNRSWHKVAEAVSSPAGVGVTWLEPDYQVYLNASKVPGEADDPTELACRVVDTKSGEANVRFT
 VSWYYRMNRRSDNVVTSELLAVMDGDWTLKYGERSKQRAQDGDFTFSKEHTDTFNFRIGRTTEEDRGNYICVVS
 AWTQKQNNNSWVSKDVFSPFNITWALEDSVLVVKARQPKPFFAAGNTFEMTCKVSSKNIKSPRYSVLIMAEKP
 VGDLSPPNETKYLLISLDQDSVVKLENWTDASBVDGVVLEKVVQEDFRYRMYQTQVSCAGLYRCNVTAWSFVRGS
 LWREAATSLSNFIETDFQTSGLPINFASVHSUTPSVIRGDLIKLFCTITVEGRALDPDDMAFDVSWFAVHSTGLD
 KAPVLLSSLDKRGIVFTSRDWSKSDLSLERVSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSPTSWQKEAEIHS
 KPVFITVKMDVLNAFKYFLIGIGLSTVIGLLSCLIGYCSSHWCKKEVQETRRERKKLMSMEMD

Signal sequence.

amino acids 1-21

Transmembrane domain.

amino acids 833-853

N-glycosylation sites.

amino acids 44-47, 286-289, 300-303, 383-386, 413-416, 525-528, 600-603,
618-621, 691-694

Tyrosine kinase phosphorylation site.

amino acids 632-640

N-myristoylation sites.

amino acids 243-248, 398-403, 511-516, 651-656, 753-758, 789-794, 836-841,
844-849

Cell attachment sequence.

amino acids 703-705

Immunoglobulin domain.

amino acids 36-121, 162-249, 292-375, 422-517, 564-657, 704-795

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FIGURE 137

MSRSRHLGKIRKKLEDVKSQWVRPARADFSDNESARLAFDALIDGGSEAYWRVLSQEGEVDFLSSVEAQYIQAAQ
AREPPCFFDTLGGAEAGPKGLDSSSLQSGTYFFVASEGSEFALLNSWASAEKPYLKEKSSATVYFQTVKHMNIR
DLVRRICITRTSQVLVILMDVFTDVEIFCDILEAANKRSGVFVCVLLDQGGVKLEQEMCDKVQISDSHLKNISIRS
VEGEIYCAKSGRKFAQQIREKFILSDWRFVLSGYSFTWLCGHVHRNLSKFTGQAVELFDEEPRHLYASSKPV
MGLKSPRLVAFVPPGAAPANGRLSSSSGASDRTSSNFFSGPSAGSHPTESVVSASSGPCSFAPHPPPPPRFQ
PHQGPWGAPSPQARLSRPHDGPFAAVYSNLGAYRFTKLQLEQLGLVERLTFTWRPFLQASPEF

Transmembrane domain.

amino acids 154-175

N-glycosylation sites.

amino acids 32-35, 217-220

Tyrosine kinase phosphorylation site.

amino acids 221-228

N-myristoylation sites.

amino acids 45-50, 86-91, 94-99, 112-117, 186-191, 311-316, 341-346

Amidation site.

amino acids 232-235

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FIGURE 138

MALPQPPPPAGARDPVTPEHWASGPPSQAPQLLRQEAKEEEEGETGVQGANGTGTAEQPPRGWGEAAESAAAE
 EGQAEVGGAAAAGSSGSPAGGAGGGGCGSWRPLLAWLORRQPQCCPCAAPLSBSAAHCCHGGTKMAALAYNLGKRE
 INHYFSVRSKVLALVAVLLLAACHLASRRYRGNDGCEYLLSSGRFLGKQVWQPHSCMMHFKISEAKNCLVDK
 HIAFIGDSRIRQLFYSFVKIINPQPKBECNKHENIPFEDKTASVKVDFLWHPEVNGSMKQCIKVTEDSIAKPH
 VIVAGATWSIKIHNGSSEALSQYRMNITSIAFLLEKLAKTSUVYVWLQDPVYEDLLSENKMKMITNESTDAYNE
 AAVSILNSSTRNSKSNVKNFVSVKLIAQETIMESLDGLHLFESSRETTAMILMNVCNKILKPVDSGCCQPRFP
 VTLIQKLAACFFFLSIIGYLIFYIIHRNAHRKNKPKCTDLESGEKKNIINTPVESLEILLQSFCIKGLIMAYFY
 MCDRANLFMKENKPYTHSSFFIPIIYILVGVFYNENTKETHVLNREQTDEWKGWMLVILIYHISGASTFLPV
 YMHIRVLVAAYLFTQGYGHFSYFWIKGDFGLYRVCQVLFRLNFLVVLCTVMDRFYQFYFVPLVTVMFVIYV
 TLALWFOIILQKANGNCFWHFGLLDLGLGFLLLFTICFLAYSQCAFEEKIFSLWPLSKCFELKGNVYEWFRWRLDR
 YVVFHGMLEAFIYLLALQKQILSESGGEFLFSNKISNFFLFISVVSFLTYSIWASSCKNKAECNELNPSVSVVQ
 TLAFILIRNIPGYARSVYSSFFAWFGKISLELEFICQYHIWLAADFRGILVLIPGNFMLNIIVSTFIIVCVAHET
 SQITNDLAQIIIPKDNSSLLKRLACIAAFFCGLLILLSSIQDKSKH

Transmembrane domains.

amino acids 153-173, 447-467, 495-515, 532-552, 577-597, 624-644, 651-671,
 677-697, 693-713, 733-753, 771-791, 808-828, 866-886, 904-924

N-glycosylation sites.

amino acids 182-185, 277-280, 311-314, 323-326, 377-380, 904-907

Tyrosine kinase phosphorylation site.

amino acids 180-187

N-myristoylation sites.

amino acids 47-52, 50-55, 53-58, 81-86, 82-87, 89-94, 93-98, 94-99, 96-101,
 97-102, 134-139, 181-186, 312-317, 511-516, 549-554, 746-751

Amidation site.

amino acids 144-147

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FIGURE 139

MYHCHSGSKPTEKGANEYAYANWKLCSASAICFIFMIAEVVGSHIAGSLAVVTDAAHLLIDLTSFLLSLFSLWL
SSKPPSKRLTFGWHRAEILGALLSILCIWVVTGVLVYLACERLLYPDYQIQATVMIIVSSCAVAANIVLTVVLH
QRCLGHNHKEVQANASVRAAFVHALGDLFQSISVLISALITTYFKPEYKIADFICTFIFSILVLASTITILKDFS
ILLMEGVPKSLNYSGVKELILAVDGVLSVHSLHWSLTMNQVILSAHVATAASRDSQVVRREIAKALSKSFTMH
SLTIQMESPVDQSPDCFLCEDPCD

Transmembrane domains.

amino acids 53-73, 91-111, 127-147, 166-186, 202-222

N-glycosylation sites.

amino acids 162-165, 234-237

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 81-84

Tyrosine kinase phosphorylation site.

amino acids 13-20

N-myristoylation sites.

amino acids 7-12, 42-47, 94-99, 228-233

Cation efflux family.

amino acids 78-306

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FIGURE 140

MVLSVPVIALGATLGTATSTLALCGVTCLCRSMHFKKGLLPRDQDPDLKAKPSLLGSAQQFNVKKSTEPVQFR
ALLKEFDIYGPRPAVTAPEVINIYADYSLRSTEEPTAPASPPQPPNDSRLKRQVTEELFILPQNGVVEDVCVMTW
NPEKAASWNQAPKLHYCLDYDCQKAHLFVTRLEAVTSNHGGGDCYVQGSVANRTGSVEAQTALKKRQLTTWE
EGLVLPLAEEELPTATLTTLRTCDRFSRHSVAGELRLGLDGTSVPLGAAQWGEIKTSAKEPSAGAGEVLLSIS
YLFAANRLLVVLIRAKNLHSHNQSKELLGKDVSVKVTCLKHQARKLKKKQTERAKHKINFEVNNEMINFELPDOLLQ
ASSVELEVLQDDSGQSCALGHCSLGLHTSGSERSHWEEMLKNPRQIAMNHQLHL

Signal sequence.

amino acids 1-24

Transmembrane domain.

amino acids 4-24

N-glycosylation sites.

amino acids 118-121, 201-204, 317-320

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 65-68, 342-345

N-myristoylation sites.amino acids 11-16, 15-20, 189-194, 197-202, 204-209, 261-266, 380-385,
385-390, 396-401, 401-406**C2 domain.**

amino acids 304-394

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FIGURE 141

MQKIMSIISVLLSFVLWGLIFGVSSNSIQIGGLFPPGADQEYSAPKVGQVQFSTSEFRLTFPHIDNLEVANSFAVT
 NAFCSQPSKRGVYAIFFGYDKESVNTITSGCGTLHVSFITPSFPTDGTHTPFVIQMRPDLKGALLSLIEYYQWDKE
 AYLYDSDRGLSTLQAVLDSAAEKKEWQVTAINVGNINNDKKDEMYRSLFQDLELKKERRVILDCERDKVNDIVDQ
 VITIGKHVKGYRTIANLEFTDGDLLKIQFGGANVSGFQIVDYDDSLVSKFLERWSTLEEKEYFGANTTTIKYT
 SALTYPDVAQVMTAFRNLRKQRIEISRRGNAGDCLANPAVPWGGQGVETIERALKQVQVEGLSGNIKFDQNGKRIN
 YTIMIMELEXTNGPRKIGYWSEVCKMVVILTELPSCGNDTSGLENKTVVVTITLESPIVMMKKKNHEMLEGNERYEC
 YCVDLAANIARKHCSFKYKLTIVGDGKYGARDADTKIWNMGVGEIVYCKADIAIAFLTITLVREEVIDFSKPFMS
 LGTISIMIKKPQSKSPGVFSFLDPLAYETWCTVFAYIGVSVVLFLVSRFSPYEWHTTEEFEDGRETQSSESTNEF
 GIFNSLWFSIGAFMRQGCDISPRSLSGRIVGGVWVFFTLIISSYTANLAAFLTVERMVSPITESAEDLSKQTEI
 AYGTLDGGSTKEFFRRSKIAVFQKMTYMRSAEPSVFVNTTAEQVARVRKSKOKYAYILLESTMNEXTEQREKPCD
 TMKVGGNLDSKEYGIATPKGSSSLGTPVNLAVLKLSEQGVLDKLNKOWYDKGECGAKDSSGSRKRTSALSLSNVA
 GVFIYLVGGGLGLAMLVALIEFCYKSPAEAKPMKVAKNAQNINPSSSQNSQNFATYKEGYNVYGLIESVKI

Signal sequence.

amino acids 1-21

Transmembrane domains.

amino acids 4-24, 543-563, 624-644, 811-831

N-glycosylation sites.

amino acids 256-259, 370-373, 406-409, 413-416

Tyrosine kinase phosphorylation sites.

amino acids 35-41, 662-667

N-myristoylation sites.
 amino acids 17-22, 21-26, 134-140, 181-186, 254-259, 287-292, 355-360,
 405-410, 472-477, 593-598, 669-674, 746-751, 760-765, 764-769, 795-800,
 823-828
Amidation site.

amino acids 365-369

Ligand-gated ion channel.

amino acids 543-834

Receptor family ligand binding region.

amino acids 56-398

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FIGURE 142

MATTVPDSCENGLKSKYYRLCDKAEANGIVLETVATAGVVTSAFMLTLFVLVCKVQDSERRKMLPTQFLFLAG
VLGIFGLTFAFIIGLDGSGTPTRFFLFGILFSICFSCLLAHAVSLTKLVGRKPLSLIVILGLAVGFSIVQDVI
ALEYIVLTMNRTNVNVFSELSAPPRNEDFVLLLTYYVLFLMALTFLMSSFTFCGSFTGWRHGAHIYLTMLLSIA
IIVAWITLIMLPDFDRWDDTILSSALAANGWVFLLAYVSPFVLLTKQRNPMDYPVEDAFCKPQLVKKSYGVE
NKAYSQGEITQGFEETGDTLYAPYSTHFCQLNQPPQKEFSIPRAHAWPSFYKDYEVKKEGS

Transmembrane domains.

amino acids 30-50, 66-86, 98-118, 121-141, 137-157, 174-194, 212-232, 244-264

N-glycosylation site.

amino acids 158-161

N-myristoylation sites.

amino acids 8-13, 38-43, 80-85, 88-93, 102-107, 136-141, 201-206

Amidation site.

amino acids 124-127

7 transmembrane receptor.

amino acids 27-273

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FIGURE 143

MLPAQEAAANLYSTNYVENSRAIGVLWAIPTICFAIVNVVCFIQFYWIGDGVDTFQAGYFGLFRHYCIGNGFSREL
TCRGSFTDFSTLPSGAFKAASFFIGLSMMLIIACIICFTLFFFCNTATVYKICAWMQLTSAACIVLGCMIFFDG
WDSDEVKRMCGEKTDKYTLGACSVRWAYILAIIGILDALILSFLAFVLGNRQDSLMABELKAENKVLISQYSLF

Transmembrane domains.

amino acids 21-41, 93-113, 127-147, 173-193

N-myristoylation sites.

amino acids 23-28, 67-72, 89-94, 182-187

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FIGURE 144

MPGAAAAAAAAAAMLPAQEAAKLYNTRYVNRNSRAIGVLWAIPTICFAIVNVVCFIQPYWIGDGVDTFQAGYFG
LFHYCIGNGFSRELTGRGSFTDFTLPSGAFKAASFFIGLSMMLIACIICFTLFFFCNTATVYKICAWMQLTS
AACLVLCMIFFPDGWDSDVEVRMCGEKTDKYTLGACSVRMAYTLAIIGILDALILSFLAFVLGNFQDSLMAEEL
KAENKVLLSQYSLE

Transmembrane domains.

amino acids 1-15, 34-54, 107-127, 141-161, 187-207

N-myristoylation sites.

amino acids 3-8, 37-42, 81-86, 103-108, 196-201

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FIGURE 145

MPGAAAAAAAAAAMLEPAQEAAKLYHTNYVRNSRAIGVLMWIFTICFAIVNVVCFIQPYWIGDGVDTFQAGYFG
LFHYCIGNGFSREITCRGSFTDFSTLPSGAFKAASFFIGLSMMLIIACIICFTLEFFCNRTAVYKICAWMQITS
AACLVLGCMIFPDGWDSDVKRMCGEKTDKYTLGACSVRWAYILAIIGILDALILSFLAFVLGNRQDSLMABEEL
KAENKVLLSQYSLE

Transmembrane domains.

amino acids 1-15, 34-54, 107-127, 141-161, 187-207

N-myristoylation sites.

amino acids 3-8, 37-42, 81-86, 103-108, 196-201

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FIGURE 146

RPLRLPCRGPRAAGTVSSESLGHPAPGQVTNRSPQFFMELFQSSPRPFLQPVVCPCGLELCDFPHRLAFSMGAG
LFSVVGTELLLPGLAALVQDWRLQGLGALMSGLLLLFWGFPALFPESPWLLATGQVARARKILWRFAEASGVG
PGDSSLEENSLATELTMLRSRSPQFRYHSPFLGLLRTVTWRNGLILGFSSSLVGGGIRASFRSLAPQVTFYLP
YFLEAGLEAAALVFLLLTADCCGRPPVLLLTMTNVPGLASLLLLAGAQYLPQWTVLFLSVLGLLASKAVSALSSL
FAAEVEPTVIRGAGLGLVLGAGFLQQAAGPLDTLHGRQGFLLQQVVFASLAVLALLCVLLLPESRSRSLPQSLQ
DADRLRRSPILLRCRPRQDHLPLEPPSNSYWAGHTPEQH

Transmembrane domains.

amino acids 67-87, 102-122, 220-240, 249-269, 265-285, 301-321, 338-358

Glycosaminoglycan attachment site.

amino acids 145-148

N-myristoylation sites.

amino acids 14-19, 27-32, 57-62, 101-106, 146-151, 180-185, 191-196, 202-207,
203-208, 228-233, 253-258, 283-288, 308-313, 312-317, 364-369

Amidation site.

amino acids 244-247

Leucine zipper pattern.

amino acids 96-117

Sugar transport proteins.

amino acids 117-126, 241-253, 276-321

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FIGURE 147

MPFEQCHLSWKNVPRPLYNAVSKELVGEFLQFVQLDKEASDPFSLNELLDELSSRKQKEELWQRLKMLLTDLVLLS
 PVDGWQVVEAQGEDNMETEHGSKMKKSIELIYAITSVILASVSVINESENYEALLECVIITNGILYALPESERK
 LQSSIQDLQCVTWWEKGLPAKEDTGKTAFAVMLLRRSLETRTGADVCLNWRINQALYCFQYDLEESGEIKDMLLEC
 FININYIKKEEGRRFLSCLFNWNINFIKMINGTIKNQLQGLQKSIMVYIABIYFRAWKKASGKILEAIENUCTQ
 DFMFHQIHLFRRSPVHASKVREVLSYFHHQKKVRQGVEMLYRLYKPILRGLKARNSEVRNAALLFVEAFFIR
 DPNLHAIEMDSKIQKQFEELYSLLEDPPYPMVRSSTGILGVCKITSKYWEMMPPTILIDLLKKVTGELAFDTSSAD
 VRCSVFCKCLPMILDNKLSPHLLLEQLLPALRYSLHDNSEKVRVAFVDMLLKIKAVRAAKFWKICPMENILVRLET
 DSRFVSRLVSLIFNSFLPVNQPREVWCERCVTLVQMNHAAARRFYQYAHHTACTNIAKLIHVIRHCLNACIQ
 RAVREFFPEDEEEEDGREKENVTVLKTLNVHDVACMAGLLEIIVILWKSIDRSMENSKKAKLYTINKFASVLP
 YLKVFQDDRCKIPLFMLMSFMPASAVPPFSCGVISTLRSREAGAVDKSYCTILLDCLCSSWGQVGHILELVDNWLF
 TEHAQAKSNTASKGRVQIRDTREVEPELALVYIEYLLTHPKNRECLLSAPRKKLHLLKALETSKADLESLLQT
 FGCKPRGFSEAAAPRAPGLHCKLSIHLQHKFCSEGVYLSMLEDTGFWLESKILSFQDQDEEDYLKLERVIYQQ
 TIQTYLTVCKDVVMVGLGDHQFQMQLLQBSLGTIMQTVKGFYVSLLLDILKEITGSSLIQKTDSDDEEVAMLLDT
 VQKVFQKMLECIARSFRKQPEEGLALLYSVQRPLHEFITAVQSRHTDTFVHRGVLSLTLAGFVVEISHQLRKVS
 DVEELAPPEHLSLELPPFSRCLIGIYIKSSNVVRSFLDELKACVASNDIEGIVCLTAAVHIILVINAGKHKSSKV
 REVAATVHRKLTFTMEITLEEDSIERFLYESSRSLGELINS

Transmembrane domain.

amino acids 1081-1101

N-glycosylation sites.

amino acids 120-123, 612-615

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 280-283, 430-433, 1033-1036

Tyrosine kinase phosphorylation sites.

amino acids 99-106, 314-321, 329-337, 385-391, 844-852

N-myristoylation sites.

amino acids 137-142, 189-194, 254-259, 262-267, 698-703, 920-925, 1015-1020

Amidation site.

amino acids 233-236

ATP/GTP-binding site motif A (P-loop).

amino acids 167-174

Leucine zipper pattern.

amino acids 128-149, 135-156, 787-808

Mitochondrial energy transfer proteins signature.

amino acids 982-990

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FIGURE 148

MEKRETFVQAVSKELVGEFLQPVQLDKEASDFFSLNELLELSRKQKEELWQRLKNNLLTDVLLSPVDGWQVVE
 AQGEDNMETERHSGSKMRKSTELIYAITSVILASVSVINESENYEALLECVIILNGILYALPESERKLSSTIQDL
 VTWWEKGLFAKEDTGKTAFAVMLLRSLSTKTGADVCLWRIRQALYCFDYDLEESGEIKDMLLECFININYIKK
 EECRRFLSCLFNWNINFIKMIHGTIKNQLQGLQKSLMVYIAEITYFRAWKKASGKILEAIENDCIQDFMTHGIHL
 FRRSPVHSKVRREVLSYFHHQKKVRQGVVEMLYRLYKPIILWRGLKARNSEVRSNAALLEVEAFFTRDPNLBAIEM
 DSRIQKQFEELYSLLEDIFYPMVIRSTGILGVCKITSKYWEMMPPTILIDLLKKVTGELAFDTSSADVRCVFKCL
 PMILDNKLSPHLLLEQLLPALRYSLHDNSEKVRVAFVDMLLKIKAVRAAKFWKICPMENILVKLETDSRPVSRRL
 VSLIFNSFLPVNQPEEVCERCVTLVQMNHAAARRFYQYASEHTACTNIAKLIHVIRECLNACIQRAVREPPED
 EEEEDGREKENVTVLDKTLVNDVACMAGLEITIVTLWKSIDRSMEMNKEAKLYTINKFASVLEPYLKVEKDDR
 CXIPLFMLMSFMPASAVPPFCGVISTLRSREEGAVDKSYCTLLDCLCSWGQVGHILELVDNWLPTENHAQAKSN
 TASKGRVQIHDTREVVKPELALVYIEYLLTHPKNRECLLSAPRKKLNHLLKALETSKADLESLLQTPGGKPERGFS
 EAAAPRAFGLNCRSLIHLQHKFCSECKVYLSMLEDTGFWLESKILSPIQDQEEDYKLHNVYQQIIQTLYLTV
 KDVVMVGLGDHGFQMQLLQBSLGIMQTVKGFFVYVSLLEDILKEITGSSLIQKTDSDDEEVAMLLDTVQKVFKML
 ECIARSFRKQPEEGLRLLYGVQRPLHEFTTAVQSRHTDFPVHGVLSSTLIAGPVVEISHQDRKVSQVEZLTPE
 HSLDLPPFSRCLIGITIKSSNVVRSFLDELKACVASNDTEGIVCLTAABVHLLVINAGKHKSSKVRVAATVHR
 KLKTFMEITLEEDSIERFLYESSSRTLGELLNS

Transmembrane domain.

amino acids 1072-1092

N-glycosylation sites.

amino acids 111-114, 603-606

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 3-6, 271-274, 421-424, 1024-1027

Tyrosine kinase phosphorylation site.

amino acids 91-97, 305-312, 320-328, 376-382, 835-843

N-myristoylation sites.

amino acids 128-133, 180-185, 245-250, 253-258, 689-694, 911-916, 1006-1011

Amidation site.

amino acids 224-227

ATP/GTP-binding site motif A (P-loop).

amino acids 158-165

Leucine zipper pattern.

amino acids 119-140, 126-147, 778-799

Mitochondrial energy transfer proteins signature.

amino acids 973-981

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FIGURE 149

MNSTLPSQVENHSHVHSNFSEENNAQLLAFENDDCHLPLAMIFTLALAYGAVILLGVSGNLALIIIIILKQKEMRNV
TNILIVNLSFSDLLVAINCLPPTFFVYTLMDHVVFGEAMCKLNPFVQCVSITVSIFSLVLLAVERHQLIINERGW
RPNNRHAYVGIATVWVLAVASSLPFLIYQVMTDEPTQNVTLDAYKDKYVCFDQFPSSDHPLSYTTLLLVLYFG
PLCFIFTCYFKIYIRLKRNNMMMDKMRDNHYRSSETKRINIMLLSIVVAFVAVCWLPITIFNTVFDWNHQIATC
NHNLLFLLCLTAMISTCVNPIFYGFLLNKNFORDLQFFNFCDPRSRDDDYETIAMSTMETGVSKESLKQASPV
AFKKINWDDNEKI

Transmembrane domains.

amino acids 38-58, 78-98, 117-137, 155-175, 208-228, 260-280, 296-316

N-glycosylation sites.

amino acids 2-5, 11-14, 17-20, 73-76, 81-84, 186-189

Tyrosine kinase phosphorylation sites.

amino acids 247-253, 341-347

N-myristoylation site.

amino acids 54-59

7 transmembrane receptor (rhodopsin family) ..

amino acids 57-320

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FIGURE 150

MVRCDKGLQMLLTAGAAFAAFSLMAIAIGTDYWLSSAHICNGSTNLTMDGGPPFRFARGDLTHSGLWVRVOCLEG
IYKGHCPRINHFPEENDYDHDSSSEYLLRIVRASSVFPILSTILLGGLCIGAGRIYSRKNMIVLSAGILFVAA
GLSNIIGIIVYISSNTGDPSPDKRDEDKKNHNYGWSFYFGALSFIVAETVGVLA VNIYIEKNKELRFKTKREPL
KASSSSPYARMPSYRYRRRRSRSSSRSTEASPSRDVSPMGLKITGAIPMGELSMYTLREPLKVTTAASYSFDQ
EASFLQVHDFFOGDLKEGFHVSMINERTTPV

Signal sequence.

amino acids 1-19

Transmembrane domains.

amino acids 103-123, 140-160, 182-202

N-glycosylation sites.

amino acids 42-45, 45-48

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 240-243, 322-325

N-myristoylation sites.

amino acids 16-21, 43-48, 74-79, 122-127, 262-267

Cell attachment sequence.

amino acids 58-60

EMP-22/EMP/MF20/Claudin family.

amino acids 6-202

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FIGURE 151

MARGFGLAPPPRLRLPLLLLVLAAVTGHTAAQDNCTCPTNEMTVCSFDSPGGRCQCRALGSGMAVDCSTLTSTKCL
LLKARMSAPKNARTLVRPSEHALVDNDGLYDPDCDFEGRFKARQCNQTSVCWCVNNSVGVRRTDEGGLSLRCDEL
VRTHHILTDLRHRPTAGAPNHSDLDAELRRLFRERYRLRPFVAADVHYEQFTIQIELRQTSQKAAGEVDIGDA
AYYFERDINGESLFGGRGGLDLRVGCEPQVERTLIYYLDEIPPKPSMKRLTAGLIAVIVVVVALVAGMAVLV
ITNRRKSGKYKKVEIKELGELRKEPSL

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 274-284

N-glycosylation sites.

amino acids 33-36, 120-123, 166-171, 209-211

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 271-274, 300-303

N-myristoylation sites.

amino acids 59-64, 132-137

Thyroglobulin type-1 repeat.

amino acids 73-145

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FIGURE 152

MGKCSGECTLVAFCCQLQVAALERQIFDFLGYQWAPILANFLHIMAVILGIFGTVQYRSRYLILYAANLVLVVG
WNAFLICFYLEVQQLSQDRDFTMTFTNTSLHRSWWMENSGGCLVTPVLNSRLALEDHHVISVTGCILDYPYIEAL
SSALQIFLALFGFVFACYVSKVFLEEDSFDFIGGFUSYGYQAPQKTSHLQLQFLYTSG

Signal sequence.

amino acids 1-21

Transmembrane domains.

amino acids 33-53, 62-82, 147-167

N-glycosylation site.

amino acids 100-103

Tyrosine kinase phosphorylation site.

amino acids 24-32

N-myristoylation sites.

amino acids 50-55, 162-167

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FIGURE 153

MEAPRAREQPRVFGERQPLLPRGARGPRRWRAAGAVALLEMLERAAPFGVTANLVLYLNSTNFWTGEQATR
AAIVFLGASYLLAPVGGWLADVYLGKRYRAVALSLLLYLAASGLLPATAFFDGRSSFCGENFASPLGPACPSAGC
PRSSPSPYCAPVLYAGLLLLGLAASSVRSNLTSEFADQVMDLGRDATRBFTNWFYWSINLGAVLSLLVVAFLQQ
NISFLLCYSIPVGCVGLAFFIFLFPATPVFITKPPMGSQVSSMLKLALQNCPPQLWQRHSARDRQCARVLADERS
PQPGASFOEDIANFQVLVKILFVMVTLVPYWMVYFQMSTYVLQGLHLNIPNIFPANEANISVALKRAQSSSYTI
FEAWLLLANVVVVLTIVELKDRLIDPLLLACKILLPSALQKMALGMFFGFTSVIVAGVLEMERLHYIHHNETVSQ
QIGEVLYNAAPLSTIWWQIPQYLLIGISEIFASIPGLEFAYSEAPRSMQGAIMGIEFFCLSGVGSLLGSSLVALLS
LPGGWLRCPKDFGRINNCRMPLYFFLLAGIQAVTALLPVWLAGRYERASQQPASHSRFSRONG

Transmembrane domains.

amino acids 35-55, 73-93, 98-118, 157-177, 199-219, 250-270, 341-361,
369-389, 408-428, 457-477, 499-519, 537-557

N-glycosylation sites.

amino acids 61-64, 66-69, 178-181, 223-226, 356-359, 439-442

Glycosaminoglycan attachment site.

amino acids 503-506

N-myristoylation sites.

amino acids 51-56, 90-95, 116-121, 147-152, 169-174, 209-214, 258-263,
365-370, 414-419, 479-484, 493-498, 497-502, 506-511, 531-536

POT family.

amino acids 101-503

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FIGURE 154

MWVNPPEVILLANALWITERANPYFILQRRKGHAGDGGGGGLAGLLVGTLDVVLDSARVAPYRILYQTPDSL
 YWFIACGGSRKEITEHWEWLEQNLLQTLSEIFENENDITTFVRGKIQGIIAEYNKINDVKEDDDTEKFKEALVKF
 HSLFGMPPEEKLVNYYSCSYWKGKVPFQCWMYLSINHLCFYSFLMGREAKLVIRWVDITQLEKNATLLLPDVIK
 VSTRSSEHFFSVFLNINETFKLMEQLANIAMRQLLDNEGFEQDRSLPKLKRKSPKKVSALKPDLDAKASERYR
 ALERLEKDEKLDGHTDCTLWTFPNKMHILQMFVSTNYICFTSKEENLCSLITFLBEVTIVEKADSSSVLPSP
 SISTNRNMTTFEANKLDRDFLVQRIEDFLQQTTSKIYSDKEFAGSYNSSDDEVYSRPSSSVSSSPQRSTSSDAD
 GERQFNNGNSVPTATQFLMTMYRRSFEEFNPKLAKFLKEQAWKINFAEYGGGICMYRTEKTRVLKGIPE
 SMRGELWLLLSGAINERATHPGYYEDIVEKSMGKYNLATEETIERDLHRSLEPSPAFQWEMGIAALRRVLTAYAF
 RNPNTIGYCOAMNIVTSVLLLYAKEEFAFWLLVALCERMLPDYVNTRVVGAALVDQGVFEELARDYVFPQLYDCMQD
 LGVISTISLSWFLTLFLSVMPFESAVVVDCCFFYEGIKVIFQLALAVLDANVDKLLNCKDDGEAMTVLGRYLDG
 VTNEGSTLPPPIPHLSLLSDDVEPYFEVDIFRLIRTSYEKFGTIPADLIRQMRFKQRLKVIQTLEDTTKRVVR
 TIVTETSFTIDELEELYALFKASHLTSCYWGSSNALDRHDPSPYLEQYRIDFEQFGMFAILLFPWACGTHSD
 VLASRLFQLLDENGDSLINFREFVSSLSAACHGDLTEKLLKLYRMSVLEPSSDQDEPOSAFEATQYFFEDITF
 ECTHVVGCLDSRSKQGADGPFVTVSLKPKDKRANSQENSNYLRLWTFPENKSKSKNAKDLPKLNQGGFIELCKTM
 YNMFSEDFNEQELYHATAAVTSILLRIGEVGKLFVAQPAKESGSSGSGSCHQGIPGVLFPRKGPQGPYVVESV
 EPLPASLAPDSEHSLGGQMEDIKLEDSSPRONGACSSMLISDDDTKDESSMSSYSVLASGSHEEDKLHCEDIG
 EDTVLVRSQGQTAALPRSTSLDRDWAITEQFLASLLTEPALVKYFDKPVCMARITSAKNIRMMGKPLTSASD
 YEISAMSG

Transmembrane domains.

amino acids 35-55, 669-689

N-glycosylation sites.

amino acids 212-215, 239-242, 417-420, 1011-1014

Glycosaminoglycan attachment site.

amino acids 1192-1195

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 372-375, 277-280, 468-471

N-myristoylation sites.

amino acids 36-41, 37-42, 39-44, 40-45, 44-49, 414-419, 497-502, 515-520,
 668-673, 782-787, 845-850, 846-851, 914-919, 977-982, 1078-1083, 1079-1084,
 1082-1087, 1144-1149, 1193-1198

Amidation site.

amino acids 991-994

TBC domain.

amino acids 512-724

S-100/ICaBP type calcium.

amino acids 691-911

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/19592

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07K 16/18, 16/30; G01N 33/374

US CL : 530/300, 350, 387.7, 387.9, 387.3, 395; 424/130.1, 133.1, 141.1, 155.1; 435/172.2, 328, 344, 390, 7.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/300, 350, 387.7, 387.9, 387.3, 395; 424/130.1, 133.1, 141.1, 155.1; 435/172.2, 328, 344, 390

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WEST, GenCore databases**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,965,710 A (BODMER et al) 12 October 1999 (12.10.1999), column 9, lines 14-19; column 10, lines 10-11; Example 6 of columns 17-19; Sequence 34 within columns 49-52 and attached database sheet.	1-9 and 12-15
Y	US 4,331,598 A (HASEGAWA et al) 25 May 1982 (25.05.1982), abstract, column 16, lines 65-68.	10 and 11

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

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document number of the same patent family

Date of the actual completion of the international search

26 May 2003 (26.05.2003)

Date of mailing of the international search report

04 JUN 2003

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